

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 3, 2003, 19:52:03 ; Search time 44 Seconds  
(without alignments)  
4074.113 Million cell updates/sec

Title: US-09-870-090A-2

Perfect score: 4577

Sequence: 1 MADSEGPAGGGEVAELPG.....PRCDGHOQYPRKWRDTPAD 870

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvillus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4573	99.9	871	4 Q9HBC0	Q9hbc0 homo sapien
2	4571	99.9	871	4 Q9HBA0	Q9hba0 homo sapien
3	4570	99.8	871	11 Q96092	Q96q92 mus musculus
4	4393	96.0	871	11 Q9EPK8	Q9epk8 mus musculus
5	4387	95.8	871	11 Q9EP76	Q9ep76 mus musculus
6	4378	95.7	871	11 Q9ER28	Q9er28 rattus norv
7	4374	95.6	871	11 Q9EQ24	Q9eq24 mus musculus
8	4334	94.7	873	11 Q9ER27	Q9er27 mus musculus
9	4220	92.2	803	4 Q96RS7	Q96rs7 homo sapien
10	4087	89.3	803	11 Q91XR5	Q91xr5 mus musculus
11	3831.5	83.7	852	13 Q9DF53	Q9dfs3 gallus gall
12	1849	40.4	843	13 Q9QFN9	Q9qfn9 gallus gall
13	1819	39.7	838	11 Q9JMS7	Q9jms7 rattus norv
14	1818	39.7	838	11 Q35433	Q35433 rattus norv
15	1800	39.3	839	4 Q9NQ74	Q9nq74 homo sapien
16	1799	39.3	839	4 Q9NY22	Q9ny22 homo sapien

17 1795 39.2 839 4 Q9H304  
18 1795 39.2 839 4 Q9H0G9  
19 1693.5 37.0 528 11 Q92182  
20 1607.5 35.1 778 11 Q9JMS6  
21 1549 33.8 312 11 Q9CW94  
22 1497.5 32.7 761 11 Q9WUD2  
23 1495.5 32.7 761 11 Q9QVH8  
24 1491 32.6 762 11 Q9JMI8  
25 1469.5 32.1 756 11 Q9WTR1  
26 1469.5 32.1 756 11 Q99K71  
27 1467 32.1 764 4 Q9Y5S1  
28 1459 31.9 721 11 Q9CVC7  
29 1454.5 31.8 764 4 Q9Y670  
30 1071 23.4 511 4 Q9H303  
31 1041 22.7 468 11 Q92084  
32 1016 22.2 471 11 Q9JLM0  
33 764.5 16.7 727 11 Q91WD2  
34 757.5 16.6 727 11 Q9R186  
35 753.5 16.5 725 4 Q9H296  
36 753.5 16.5 725 4 Q9H1D0  
37 752.5 16.4 725 4 Q9H1D1  
38 744.5 16.3 730 6 Q9XSM3  
39 742 16.2 729 4 Q9NOA5  
40 735.5 16.1 723 11 Q9JUL2  
41 730.5 16.0 723 11 Q9JIF0  
42 598.5 13.1 557 4 Q8TDL3  
43 584.5 12.8 729 11 Q9JJJ0  
44 503.5 11.0 937 5 Q17469  
45 486.5 10.6 769 5 Q9N3Y9

#### ALIGNMENTS

RESULT 1

Q9HBC0 PRELIMINARY; PRT; 871 AA.

ID Q9HBC0  
AC Q9HBC0;  
DT 01-MAR-2001 (TREMREL. 16, Created)  
DT 01-MAR-2001 (TREMREL. 16, Last sequence update)  
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)  
DE CTRPC4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=KIDNEY CORTEX;

RX MEDLINE=20482174; PubMed=11025659;

RA Strotmann R., Harteneck C., Nunnemacher K., Schultz G., Plant T.D.;  
RT "OTRPC4, a nonselective cation channel that confers sensitivity to  
RT extracellular osmolarity.";

RL Nat. Cell Biol. 2:695-702(2000).

DR EMBL; AF258465; AAG16127.1; -;

DR InterPro; IPR002110; ANK.

DR InterPro; IPR000636; M-channel\_trpL.

DR InterPro; IPR004729; Trp\_Cachannel.

DR Pfam; PF00023; ank; 3.

DR Pfam; PF00520; ion\_trans; 1.

DR SMART; SM00248; ANK; 3.

DR TIGRFAMS; TIGR00870; trp; 1.

DR PROSITE; PS50088; ANK\_REPEAT; 1.

DR PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.

DR ANK repeat; Repeat.

KW ANK repeat; Repeat.

SQ SEQUENCE 871 AA; 98294 MW; C6205686DEA6FB6 CRC64;

Query Match 99.9%; Score 4573; DB 4: Length 871;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 869; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGGEVAELPGDESGTGGGAFFPLSSLANLFEEDGSLSPADASRPAGP 60

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Db      1  MADSSGPRAGPGEVAELPGDESGTGCGEAFPLSSLANLFEDEGSLSPADSRPAGP 60
Qy      61  GDGRPNLRKMFQGAFRKGVNPNIDLLESTLYESSVVPKPKAPMDSLFDTGYTHRHSSDN 120
Db      61  GDGRPNLRKMFQGAFRKGVNPNIDLLESTLYESSVVPKPKAPMDSLFDTGYTHRHSSDN 120
Qy      121  KWRKPKKIIKQPOSQPKAPAPQPPILKVFNRPIPLFDIVSRGSTADLDGLLPFLTHKKRL 180
Db      121  KWRKPKKIIKQPOSQPKAPAPQPPILKVFNRPIPLFDIVSRGSTADLDGLLPFLTHKKRL 180
Qy      181  TDEEFREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFRDIYYRGQT 240
Db      181  TDEEFREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFRDIYYRGQT 240
Qy      241  ALHAIERRCKHYVELLVAGADVHAQAGRRFPQKDEGGYFYFGEPLSLAACTNPHI 300
Db      241  ALHAIERRCKHYVELLVAGADVHAQAGRRFPQKDEGGYFYFGEPLSLAACTNPHI 300
Qy      301  VNYLTENPHKKADMRQDSRGNTVHLVAIAADNTRENTKFTVKMYDILLKLCARLPDS 360
Db      301  VNYLTENPHKKADMRQDSRGNTVHLVAIAADNTRENTKFTVKMYDILLKLCARLPDS 360
Qy      361  NLEAVLNNDGLSPLMAAATGKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVSSLYD 420
Db      361  NLEAVLNNDGLSPLMAAATGKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVSSLYD 420
Qy      421  LSSLDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLE 480
Db      421  LSSLDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLE 480
Qy      481  AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFNFKDLPMKKCPGV 540
Db      481  AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFNFKDLPMKKCPGV 540
Qy      541  NSLFDIGSFOLLYFIYSVLVSAALYLAGIEAYLAVMVFALVGLWMNALYFTRGLKLTG 600
Db      541  NSLFDIGSFOLLYFIYSVLVSAALYLAGIEAYLAVMVFALVGLWMNALYFTRGLKLTG 600
Qy      601  TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 660
Db      601  TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 660
Qy      661  RDETFSTFLDLFKLTIGMDLEMLSSTKYPVVFILLVYIILFVLLNMLIALMGE 720
Db      661  RDETFSTFLDLFKLTIGMDLEMLSSTKYPVVFILLVYIILFVLLNMLIALMGE 720
Qy      721  TVGVSKESKHIKLOWATTILDIERSFPVFLKAFRSGEMVTVGKSSDGTDDRWCFRV 780
Db      721  TVGVSKESKHIKLOWATTILDIERSFPVFLKAFRSGEMVTVGKSSDGTDDRWCFRV 780
Qy      781  DEVNWSHWNQNLGIINEDPGKNETYYGFSHTVGRLLRDRWSVVPVVELNKNNSNPD 840
Db      781  DEVNWSHWNQNLGIINEDPGKNETYYGFSHTVGRLLRDRWSVVPVVELNKNNSNPD 840
Qy      841  VVYPLDSMGNPCDGHQOQYPRKWRDADAP 870
Db      841  VVYPLDSMGNPCDGHQOQYPRKWRDADAP 870

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RESULT 2

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Q9HBAO  PRELIMINARY;      PRT;      871 AA.
AC      Q9HBAO;
DT      01-MAR-2001 (T-EMBLrel. 16, Created)
DT      01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DT      01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE      Vanilloid receptor-related osmotically activated channel.
GN      VROAC.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;

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RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20531888; PubMed=11081638;
RA      Liedtke W.B., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S.,
RA      Sali A., Hudspeth A.J., Friedman J.M., Heller S.;
RT      "Vanilloid receptor-related osmotically activated channel (VR-OAC), a
RT      candidate vertebrate osmoreceptor.";
RL      Cell 103:525-535(2000).
DR      EMBL: AF263323; AAC28029.1; -.
DR      InterPro: IPR002110; ANK.
DR      InterPro: IPR000636; M+channel_nlg.
DR      InterPro: IPR004729; Trp_CaChannel.
DR      Pfam: PF00023; ank; 3.
DR      Pfam: PF00520; ion_trans; 1.
DR      SMART: SM00248; ANK; 3.
DR      TIGRFAMS: TIGR00870; trp; 1.
DR      PROSITE: PS50088; ANK_REPEAT; 1.
DR      PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW      ANK repeat; Receptor; Repeat.
SQ      SEQUENCE      871 AA;  98265 MW;  A86FB6ECC9103C19 CRC64;

Query Match      99.9%; Score 4571; DB 4; Length 871;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 868; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1  MADSSGPRAGPGEVAELPGDESGTGCGEAFPLSSLANLFEDEGSLSPADSRPAGP 60
Db      1  MADSSGPRAGPGEVAELPGDESGTGCGEAFPLSSLANLFEDEGSLSPADSRPAGP 60
Qy      61  GDGRPNLRKMFQGAFRKGVNPNIDLLESTLYESSVVPKPKAPMDSLFDTGYTHRHSSDN 120
Db      61  GDGRPNLRKMFQGAFRKGVNPNIDLLESTLYESSVVPKPKAPMDSLFDTGYTHRHSSDN 120
Qy      121  KWRKPKKIIKQPOSQPKAPAPQPPILKVFNRPIPLFDIVSRGSTADLDGLLPFLTHKKRL 180
Db      121  KWRKPKKIIKQPOSQPKAPAPQPPILKVFNRPIPLFDIVSRGSTADLDGLLPFLTHKKRL 180
Qy      181  TDEEFREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFRDIYYRGQT 240
Db      181  TDEEFREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFRDIYYRGQT 240
Qy      241  ALHAIERRCKHYVELLVAGADVHAQAGRRFPQKDEGGYFYFGEPLSLAACTNPHI 300
Db      241  ALHAIERRCKHYVELLVAGADVHAQAGRRFPQKDEGGYFYFGEPLSLAACTNPHI 300
Qy      301  VNYLTENPHKKADMRQDSRGNTVHLVAIAADNTRENTKFTVKMYDILLKLCARLPDS 360
Db      301  VNYLTENPHKKADMRQDSRGNTVHLVAIAADNTRENTKFTVKMYDILLKLCARLPDS 360
Qy      361  NLEAVLNNDGLSPLMAAATGKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVSSLYD 420
Db      361  NLEAVLNNDGLSPLMAAATGKIGIFQHIIRREVTDTRHLSRKFKDWAYGPVSSLYD 420
Qy      421  LSSLDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLE 480
Db      421  LSSLDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLE 480
Qy      481  AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFNFKDLPMKKCPGV 540
Db      481  AMVIFTLTAYYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFNFKDLPMKKCPGV 540
Qy      541  NSLFDIGSFOLLYFIYSVLVSAALYLAGIEAYLAVMVFALVGLWMNALYFTRGLKLTG 600
Db      541  NSLFDIGSFOLLYFIYSVLVSAALYLAGIEAYLAVMVFALVGLWMNALYFTRGLKLTG 600
Qy      601  TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 660
Db      601  TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 660
Qy      661  RDETFSTFLDLFKLTIGMDLEMLSSTKYPVVFILLVYIILFVLLNMLIALMGE 720
Db      661  RDETFSTFLDLFKLTIGMDLEMLSSTKYPVVFILLVYIILFVLLNMLIALMGE 720

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361	Qy	NEAUVNNDGLSPLMAAAKTGKIGITFOHIIIRREVTDEDBTRHLSRKFDWAGVPVYSSLDY	420
361	Db	NEAUVNNDGLSPLMAAAKTGKIGITFOHIIIRREVTDEDBTRHLSRKFDWAGVPVYSSLDY	420
421	Qy	LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFCGAVSFYINVVSYLC	480
421	Db	LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFCGAVSFYINVVSYLC	480
481	Qy	AMVIFTLTAYOPLSGTPPYPYRTTVDYVLRAGEVITLFTGVLEFFFTNIDKLFMKKCPGV	540
481	Db	AMVIFTLTAYOPLSGTPPYPYRTTVDYVLRAGEVITLFTGVLEFFFTNIDKLFMKKCPGV	540
541	Qy	NSLFTDGSFQLLYFYISVLVIVSAALYLAGIEAVLAVMVFALVLGWNALYFTFRGLKLTG	600
541	Db	NSLFTDGSFQLLYFYISVLVIVSAALYLAGIEAVLAVMVFALVLGWNALYFTFRGLKLTG	600
601	Qy	TYSIMIQTLFKDLFRFLVLLFMIGYASALVSLNAPCANMKVCNEDQNTCTVPTYPS	660
601	Db	TYSIMIQTLFKDLFRFLVLLFMIGYASALVSLNAPCANMKVCNEDQNTCTVPTYPS	660
661	Qy	ROSEFTSTFLDLFKLTIGMGDLEMLSTKYPVVFIIILVYIITLTVLLNLMIALMGE	720
661	Db	ROSEFTSTFLDLFKLTIGMGDLEMLSTKYPVVFIIILVYIITLTVLLNLMIALMGE	720
721	Qy	TVGQVSKESKHITWKLOWATTIILDIERSPPVFLRAFRSGEMVTVGKSSDGTDPDRRCFRV	780
721	Db	TVGQVSKESKHITWKLOWATTIILDIERSPPVFLRAFRSGEMVTVGKSSDGTDPDRRCFRV	780
781	Qy	DEVNWSHNQNLGIINEDPGKNFYQYVGFSTVGRLLRDRWSSVPRVVVELNKNKNPDE	840
781	Db	DEVNWSHNQNLGIINEDPGKNFYQYVGFSTVGRLLRDRWSSVPRVVVELNKNKNPDE	840
841	Qy	VVVPVLDMSGNPRCDGHQOQYPRKWRITDDAP	870
841	Db	VVVPVLDMSGNPRCDGHQOQYPRKWRITDDAP	870

ID	Q9EPK8	PRELIMINARY;	PRT;	871 AA.
AC	Q9EPK8;			
DT	01-MAR-2001	(TrEMBLrel. 16, Created)		
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)		
DT	01-JUN-2002	(TrEMBLrel. 21, Last annotation update)		
DE	Transient receptor potential protein 12.			
GN	TRPV4 OR OTRPC4 OR TRP12.			
OS	MUS MUSCULUS (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; E			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; M			
OX	NCBI_TaxID=10090;			
RI	[1]			
RN	SEQUENCE FROM N. A.			
RP	TISSUE=KIDNEY;			
RC	TX	MEDLINE=20547522; Pubmed=11094154;		
RT	Wassenbach U., Boedding M., Freichel M., Flockerzi V.			
RA	"Trp12", a novel Trp related protein from kidney."			
RL	FEBS Lett. 485:127-134(2000)			
DR	EWBL; AJ296078; CAC20703.1;			
DR	MGD; MG1:1926945; Trpv4.			
DR	InterPro; IPR002110; ANK.			
DR	InterPro; IPR002111; Cat_channel_TrlP.			
DR	InterPro; IPR000636; M-channel_nlg.			
DR	InterPro; IPR004729; Trp_CaChannel.			
DR	Pfam; PF00023; ank; 3.			
DR	Pfam; PF00520; Ion.trans; 1.			
DR	SMART; SM00248; ANK; 3.			
DR	TIGRFAMs; TIGR00870; ank; repeat: 1.			
DR	PROSITE; PS50088; ANK_REPEAT; 1.			
DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.			
DR	ANK repeat; Receptor; Repeat.			
SW	SEQUENCE 871 AA; 98026 MW; 58ACGE33F89CEA05 CRC64; M			

DE	transient receptor potential protein 12.
DN	TRPV4 OR TRPC4 OR TRP12.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
OX	[1] NCBI_TaxId=10090;
RN	SEQUENCE FROM N.A.
RP	TISSUE=KIDNEY;
RC	MEDLINE=20547522; PubMed=11094154;
RX	Wissenbach U., Boedding M., Freichel M., Flockerzi V.;
RT	"Trp12, a novel Trp related protein from kidney.";
RL	FEBS Lett. 485:127-134 (2000).
DR	EMBL; AJ296078; CAC20703.1; .
DR	MGD; MGI:1926945; Trpv4.
DR	InterPro; IPR002110; ANK.
DR	InterPro; IPR002111; Cat_channel_TrpL.
DR	InterPro; IPR000636; M-channel_nlg.
DR	InterPro; IPR004729; Trp-CaChannel.
DR	Pfam; PF00023; ank; 3.
DR	Pfam; PF00520; Ion_trans; 1.
DR	SMART; SM00248; ANK; 3.
DR	TIGRFAMS; TIGR00870; trp; 1.
DR	PROSITE; PS50088; ANK_REPEAT; 1.
DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR	ANK repeat; Receptor; Repeat.
SW	SEQUENCE 871 AA; 98026 MW;
KQ	5BAC6E33F99CEAA05 CRC64;







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Db 481 LCAMVFTLTAAYOPELEGPPYRTVDYLRAGEVITLFTGVLFEEFSIKDLFTKKCP 540
QY 539 GVNSLFDGSGFLLYFIYSVLIVSAALYLAGIAYLAVMVFALVGLWNNALYFTGLKL 598
Db 541 GVNSLFDGSGFLLYFIYSVLIVSAALYLAGIAYLAVMVFALVGLWNNALYFTGLKL 600
QY 599 TGYSTMIQIKFLKDLFRLLVYLLFMIGYASALVSLNCPANKVCNEDQTNCTVPTYP 658
Db 601 TGYSTMIQIKFLKDLFRLLVYLLFMIGYASALVSLNCPANKVCNEDQTNCTVPTYP 660
QY 659 SCRDSEFTFLDLKFLTGMDLEMLSTKYPVVFIIILLYTYIILTFVLLNMLIALM 718
Db 661 ACRDSEFTFAFLDLKFLTGMDLEMLSAKYPVVFIIILLYTYIILTFVLLNMLIALM 720
QY 719 GETVGQVSKESHIWKLQATNLTIDERSFPVFLKAFRSGEMVTVGKSSDGTDDRWC 778
Db 721 GETVGQVSKESHIWKLQATNLTIDERSFPVFLKAFRSGEMVTVGKSSDGTDDRWC 780
QY 779 RVDEVNWSHWNQNLGIINEDPGKNEYQYGFSGHTVGRLLRRDRWSSVPRVVELNKN 838
Db 781 RVDEVNWSHWNQNLGIINEDPGKSEYQYGFSGHTVGRLLRRDRWSSVPRVVELNKN 840
QY 839 DEVVPLDSMGNPCDGHQGYPRKWRDAP 870
Db 841 DEVVPLDNLGNPCDGHQGYAPKWRDAP 872

RESULT 9
Q9RS7 PRELIMINARY; PRT; 803 AA.
AC Q96RS7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vanilloid receptor-like protein 2.
GN VRL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Derst C., Schafer M.K.;
RT "Cloning of mouse and human vanilloid receptor-like protein 2 (VRL-2).";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF279673; AAK69487.1; -.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000636; M+channel_nlg.
DR InterPro: IPR004729; Trp_CaChannel.
DR Pfam: PF00023; ank_3.
DR Pfam: PF00520; ion_trans_1.
DR TRIGRAMS; TIGR00870; trp; 1.
DR PROSITE; PS0088; ANK_REPEAT; 1.
DR PROSITE; PS0297; ANK_REPEAT; 1.
KW ANK repeat. Receptor. Repeat.
SQ SEQUENCE 803 AA; 91635 MW; AB329C595B325784 CRC64;

Query Match 92.2%; Score 4220; DB 4; Length 803;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 802; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 MKFOGAFKGVNPNIDLESTLYESSVPGPKAPMDSLFDTYRHHSSDNKRWRKKII 128
Db 1 MKFOGAFKGVNPNIDLESTLYESSVPGPKAPMDSLFDTYRHHSSDNKRWRKKII 60
QY 129 EKQOSPAPAPQPPILKVFNRPIFLDIVSGSTADLDGLLPFLLTTHKKRLTDEEF 188
Db 61 EKQOSPAPAPQPPILKVFNRPIFLDIVSGSTADLDGLLPFLLTTHKKRLTDEEF 120
QY 189 STGKTCPLKALLNLNGRNDTIPVLLDIAERTGNMREFINSPRDIYRGOTALHIA 248
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Db 121 STGKTCPLKALLNLNGRNDTIPVLLDIAERTGNMREFINSPRDIYRGOTALHIA 180
QY 249 RCKHYVELLVAQADVAQARGFPQKDEGGYFYFGEPLSLAACTNPHIVNYLTENP 308
Db 181 RCKHYVELLVAQADVAQARGFPQKDEGGYFYFGEPLSLAACTNPHIVNYLTENP 240
QY 309 HKKADMRRODSRGNTVLHALVAIADNTRENTKFTKMYDLLLLLKCARLPDPSNLEAV 368
Db 241 HKKADMRRODSRGNTVLHALVAIADNTRENTKFTKMYDLLLLLKCARLPDPSNLEAV 300
QY 369 DGLSPLMAAKTKGKIGIFQHIIRREVTDETRHLSRKFWDWAYGPPYSSLYDSSLDTC 428
Db 301 DGLSPLMAAKTKGKIGIFQHIIRREVTDETRHLSRKFWDWAYGPPYSSLYDSSLDTC 360
QY 429 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSVLCAMVFTLT 488
Db 361 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSVLCAMVFTLT 420
QY 489 AYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGVNSLFD 548
Db 421 AYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGVNSLFD 480
QY 549 FOLLFYIYSVLVISAAALYLAGIAYLAVMVFALVGLWNNALYFTGLKLGTYSIMIQ 608
Db 481 FOLLFYIYSVLVISAAALYLAGIAYLAVMVFALVGLWNNALYFTGLKLGTYSIMIQ 540
QY 609 ILFKDLFRLLVYLLFMIGYASALVSLNCPANKVCNEDQTNCTVPTYPSCRDSEFT 668
Db 541 ILFKDLFRLLVYLLFMIGYASALVSLNCPANKVCNEDQTNCTVPTYPSCRDSEFT 600
QY 669 FLDDLKFLTGMDLEMLSTKYPVVFIIILLYTYIILTFVLLNMLIALMGETVGVSKE 728
Db 601 FLDDLKFLTGMDLEMLSTKYPVVFIIILLYTYIILTFVLLNMLIALMGETVGVSKE 660
QY 729 SKHIWKLQATNLTIDERSFPVFLKAFRSGEMVTVGKSSDGTDDRWCFRVDEVNWSH 788
Db 661 SKHIWKLQATNLTIDERSFPVFLKAFRSGEMVTVGKSSDGTDDRWCFRVDEVNWSH 720
QY 789 NONLGIINEDPGKNEYQYGFSGHTVGRLLRRDRWSSVPRVVELNKNPNDEVPVLD 848
Db 721 NONLGIINEDPGKNEYQYGFSGHTVGRLLRRDRWSSVPRVVELNKNPNDEVPVLD 780
QY 849 GNPDCDGHQGYPRKWRDAP 870
Db 781 GNPDCDGHQGYPRKWRDAP 802

RESULT 10
Q91XR5 PRELIMINARY; PRT; 803 AA.
AC Q91XR5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vanilloid receptor-like protein 2.
GN TRPV4 OR VRL2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY, BRAIN, AND HEART;
RA Derst C., Schafer M.K.;
RT "Cloning of mouse and human vanilloid receptor-like protein 2 (VRL-2).";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF279672; AAK69486.1; -.
DR MGD; MGI:1926945; Trpv4.
DR InterPro: IPR002110; ANK.
DR InterPro: IPR002111; Cat_channel_nlg.
DR InterPro: IPR000636; M+channel_nlg.
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DR InterPro: IPR004729; Trp\_CaChannel.  
DR Pfam: PF00023; ank; 3.  
DR TIGRFAMS: TIGR00870; trp; 1.  
DR PROSITE: PS50088; ANK\_REPEAT; 1.  
DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
KW ANK repeat; Receptor; Repeat.  
SQ SEQUENCE 803 AA; 91438 MW; 79A5BD9323300029 CRC64;  
  
Query Match 89.3%; Score 4087; DB 11; Length 803;  
Best Local Similarity 96.0%; Pred. No. 4.3e-309;  
Matches 770; Conservative 18; Mismatches 14; Indels 0; Gaps 0;  
  
Qy 69 MKFGAPRKGVNPIDLLSTLYESSVVGPKKAPMDSLFDTYRHHSSDNKRKKII 128  
Db 1 MKFGAPRKGVNPIDLLSTLYESSVVGPKKAPMDSLFDTYRHHSSDNKRKKVV 60  
  
Qy 129 EKQPSKAPAPPPPTIKVFNRPILFDIVSRGSTADLDGLLFLTHKKRLTDEEREP 188  
Db 61 EKQPSKAPAPPPPTIKVFNRPILFDIVSRGSTADLDGLLFLTHKKRLTDEEREP 120  
  
Qy 189 STGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQTALHIAIER 248  
Db 121 STGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQTSILHIAIER 180  
  
Qy 249 RCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQHPIVNYLTENP 308  
Db 181 RCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQHPIVNYLTENP 240  
  
Qy 309 HKKADMRQDSRGNTVHLVAIAADNTRENTKVTMYDLKLLKCARLPDLSNLEAVLNN 368  
Db 241 HKKADMRQDSRGNTVHLVAIAADNTRENTKVTMYDLKLLKCARLPDLSNLEAVLNN 300  
  
Qy 369 DGLSPLMAAKTKIGIFQHIIRREVTDETRHLSRKFKDMWAGPVYSSLDSSLDTCG 428  
Db 301 DGLSPLMAAKTKIGIFQHIIRREVTDETRHLSRKFKDMWAGPVYSSLDSSLDTCG 360  
  
Qy 429 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINVSVLCAMVFTLT 488  
Db 361 EESVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINVSVLCAMVFTLT 420  
  
Qy 489 AYTQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKCPGVNSLFDGS 548  
Db 421 AYTQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTSIKDLFTKCPGVNSLFDGS 480  
  
Qy 549 FQLLYFTYSLVTVSAALYLAGIYAVLVAVFALVGMNNAFYTRGLKLTGYTSIMIQ 608  
Db 481 FQLLYFTYSLVTVSAALYLAGIYAVLVAVFALVGMNNAFYTRGLKLTGYTSIMIQ 540  
  
Qy 609 ILKDLFRLLVLLFWIGYASALVSLNPNCAKNKVCNEDQTNCTVPTPSRDSSETFT 668  
Db 541 ILKDLFRLLVLLFWIGYASALVSLNPNCTNMKVCDEQSNCTVPTYPACRDSSETFSA 600  
  
Qy 669 FLDDLKLTGMGDLMSSTKYPVVFIILLVYIILTFVLLNMLIALMGETVGVOSKE 728  
Db 601 FLDDLKLTGMGDLMSAKYPVVFIILLVYIILTFVLLNMLIALMGETVGVOSKE 660  
  
Qy 729 SKHIWKQWATTILDIERSPPVFLKAFRSGEMVTYVCKSSDGTDDRWCPRVDEVNWSH 788  
Db 661 SKHIWKQWATTILDIERSPPVFLKAFRSGEMVTYVCKSSDGTDDRWCPRVDEVNWSH 720  
  
Qy 789 NQNLGIINDPGKNEYQYGFSTYGRRLRRDRWSSVPRVVELNNSNPDEVVPLDSM 848  
Db 721 NQNLGIINDPGKSEIYQYGFSTYGRRLRRDRWSSVPRVVELNNSNDADEVVPLDNL 780  
  
Qy 849 GNPRCGHQOQYPRKWRDTPDAP 870  
Db 781 GNPNCGHQOQYAPKWRDTPDAP 802

RESULT 11

Q9DFS3

ID Q9DFS3

PRELIMINARY; PRT; 852 AA.

AC Q9DFS3;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Vanilloid receptor-related osmotically activated channel protein.  
GN VR-OAC.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=COCHLEA;  
RX MEDLINE=20531888; PubMed=11081638;  
RA Lledcke W., Choe Y., Marti-Renom M.A., Bell A.M., Denis C.S., Sali A.,  
RA Hudspeth A.J., Friedman J.M., Heller S.;  
RT "Vanilloid Receptor-Related Osmotically Activated Channel (VR-OAC), a  
RT Candidate Vertebrate Osmoreceptor.";  
RL Cell 103:525-535(2000).  
DR EMBL: AF261883; AAG28026.1; -.  
DR InterPro: IPR002110; ANK.  
DR InterPro: IPR002111; Cat\_channel\_TrpL.  
DR InterPro: IPR000636; M+channel\_nlg.  
DR InterPro: IPR002016; Peroxidase.  
DR InterPro: IPR001865; Ribosomal\_S2.  
DR InterPro: IPR004729; Trp\_CaChannel.  
DR Pfam: PF00023; ank; 3.  
DR Pfam: PF00520; Ion\_trans; 1.  
DR SMART: SM00248; ANK; 3.  
DR TIGRFAMS: TIGR00870; trp; 1.  
DR PROSITE: PS50088; ANK\_REPEAT; 1.  
DR PROSITE: PS50297; ANK\_REPEAT\_REGION; 1.  
DR PROSITE: PS00436; PEROXIDASE\_2; UNKNOWN\_1.  
DR PROSITE: PS00962; RIBOSOMAL\_S2\_1; UNKNOWN\_1.  
KW ANK repeat; Receptor; Repeat.  
SQ SEQUENCE 852 AA; 96197 MW; E85365D3FADD08C1 CRC64;  
  
Query Match 83.7%; Score 3831.5; DB 13; Length 852;  
Best Local Similarity 84.7%; Pred. No. 3.6e-289;  
Matches 724; Conservative 57; Mismatches 65; Indels 9; Gaps 3;  
  
Qy 17 ELPGDESGTPGGGAFLPSSLANLFEDEGDSLSPADASR-PAGPDGRNLRMKFGAF 75  
Db 5 EDRDAGDVLGDDSFPLSSANLFEVED---TSPAPSRGPPGAGDGNLRMKFGAF 61  
  
Qy 76 RKGVPNPIDLLSTLYESSVVGPKKAPMDSLFDTYRHHSSDNKRKKRIIEKQPSQ 135  
Db 62 RKGPPRMELLESTLYESSVVGPKKAPMDSLFDTYRQHPSENKRRRRVVEKPVAGT 121  
  
Qy 136 KAPAPPPPIKVFNPILFDIVSRGSTADLDGLLFLTHKKRLTDEEREPSTGKTCL 195  
Db 122 KGPAPPPPIKVFNPILFDIVSRGSPDGLGLLFLTHKKRLTDEEREPSTGKTCL 181  
  
Qy 196 PKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQTALHIAIERCKHYVE 255  
Db 182 PKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQTALHIAIERCKHYVE 241  
  
Qy 256 LLVAQADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQHPIVNYLTENPHKKADMR 315  
Db 242 LLVEKADVHAQARGFFQPKDEGGYFYFGEPLSLAACTNQHPIVNYLTENPHKKADLR 301  
  
Qy 316 RQDSRGNTVHLVAIAADNTRENTKVTMYDLKLLKCARLPDLSNLEAVLNDGLSPLM 375  
Db 302 RQDSRGNTVHLVAIAADNTRENTKVTMYDLKLLKCARLPDLSNLEAVLNDGLSPLM 361  
  
Qy 376 MAAKTKIGIFQHIIRREVTDETRHLSRKFKDMWAGPVYSSLDSSLDTCGEASVLE 435  
Db 362 MAAKTKIGIFQHIIRREVTDETRHLSRKFKDMWAGPVYSSLDSSLDTCGEASVLE 421  
  
Qy 436 ILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYINVSVLCAMVFTTAYVQPLE 495  
Db 422 ILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYISVSVLCAMVFTTAYVQPLE 481



QY 496 GTPPYRTVDYLRAGEVITLFTGVLEFFFTNIKDLFMKKCPGVNSLFDIGSFQLLYFI 555  
Db 482 GPPPYRTTIDYLRAGEITLTLTGILFFESNIKDLFMKKCPGVNSFFDIGSFQLLYFI 541  
QY 556 YSVLVISAAIYLAGEIAYLVAVFALVGLWGNALYFTRGLKLTGYSTMIQILFKDLF 615  
Db 542 YSVLVIVTAGLIGGVEAYLVAVFALVGLWGNALYFTRGLKLTGYSTMIQILFKDLF 601  
QY 616 RFLVYLLFMIGYASALVSLNCPANMKVCNEDOTNCTVPTPCSRDSETFSTFLDLFK 675  
Db 602 RELVYLLFMIGYASALVSLNCPSPSESCSEDSHNSCTLPTVPCSRDSETFSTFLDLFK 661  
QY 676 LTIGMDLEMLSTKYPVVFIILVYIILTFVLLNMLIALMGETVGVQVSKESKIHWL 735  
Db 662 LTIGMDLEMLSAKYPGVFIILVYIILTFVLLNMLIALMGETVGVQVSKESKIHWL 721  
QY 736 QWATTILDIERSFPVFLKAFRSGEMVTYVCKSDGTDPDRRCFRVDEVNWSHWNQNLGII 795  
Db 722 QWATTILDIERSFPVFLKAFRSGEMVTYVCKSDGTDPDRRCFRVDEVNWSHWNQNLGII 781  
QY 796 NEDPGKNETYQYVGFSGHTVGLRRDRWSVPRVVELNKNNSPDEVVPLDSMGNPCDGG 855  
Db 782 SEDPGKSDYQYVGFSGHTVGLRRDRWSVPRVVELNKNNSPDEVVPLDSMGNPCDGG 841  
QY 856 HQGYPRKWRITDAP 870  
Db 842 RRHG-----QTPSSP 851

RESULT 12  
Q8QFN9 PRELIMINARY: PRT: 843 AA.  
AC Q8QFN9;  
DT 01-JUN-2002 (TremBLrel. 21, Created)  
DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)  
DE Vanilloid receptor-like protein.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=DORSAL ROOT GANGLION;  
RX MEDLINE=21842900; PubMed=11853675;  
RA Jordt S.E., Julius D.;  
RT "Molecular basis for species-specific sensitivity to 'hot' chilli peppers."  
RL Cell 108:421-430(2002).  
DR EMBL; AY072909; AAL78069.1; -.  
KW Receptor.  
SQ SEQUENCE 843 AA; 96520 MW; ABB3592C9DC179C8 CRC64;

Query Match 40.4%; Score 1849; DB 13; Length 843;  
Best Local Similarity 47.3%; Pred. No. 6e-135;  
Matches 396; Conservative 144; Mismatches 215; Indels 82; Gaps 21;

QY 41 EGEDSLSPPADASRPAGGGRPNLRMKFGCAFGRKGVNPNIDLLSTLY--ESSVPG 98  
Db 27 DGEDSAL--ETAD-----NLOGTF-----SNKVPSPKSNIFARRGFEVNG 64  
QY 99 ---PKKAPMDSLFDY-----GTYRHSSDNKRKKIKTEKQP---QSPKAPAPPPPTL 146  
Db 65 DCDKDNAPMDSFYQMDHLMAPSVIKFANMERGKLHLKLLSTDSITGCSKA-----F 116  
QY 147 KYVNPILFDIYVSRGSTDADLGLPFLTHKRLTDEEPREPSTGKTLCPKALLNSNR 206  
Db 117 KYDRRRIFDVARGSTKDLDDLlyLNRLTKHLTDDEFEKETGKTKCLLKAMLNHDGK 176  
QY 207 NDTIPVLLDIARTGNMREFTNSPFDIYYRQOTALHTAIERCKHYVELLVAQADVHA 266  
Db 117 NDTIPVLLDIARTGNMREFTNSPFDIYYRQOTALHTAIERCKHYVELLVAQADVHA 266

Db 177 NDTIPVLLDIARTGNMREFTNSPFDIYYRQOTALHTAIERCKHYVELLVAQADVHA 236  
QY 267 QARGRFQF-KDEGGYFYFEGELPSLAACNTQPHIVNLTENPHKKRRDRCRNTVL 325  
Db 237 RACGEFFRIKKGPG-FYFEGELPSLAACNTQNLQIVKFLLENPYQAADTAEDSMGMVL 295  
QY 326 HALVATADNTRNTKFTVMYDLKLLKCARLPDPSNLEAVLNNDGSLPLMAAKTKIGI 385  
Db 296 HTLVEIADNTKONTKEVTKMYNNILGAKINPILKEELTNKKGLTPLTAAKTGKIGI 355  
QY 386 FOHITREYTDDETRHLSRKFEDWAGVYVSSLYDLSLDTGCEASVLEILVYNSKIEN 445  
Db 356 FAYILDRREKIDECRHLRSRKFTEWAGPVHSSYDLSLDTGCEASVLEILVYNSKIEN 414  
QY 446 RHEMLAVEPINELLRDKWRKFGAVSFYINWVSLCAMVITFTAYVQPLE--GTPPY- 502  
Db 415 RHEMLAVEPINELLRDKWRKFGAVSFYINWVSLCAMVITFTAYVQPLE--GTPPY- 474  
QY 503 RTVDYLRAGEVITLFTGVLEFFFTNIKDLFMKKCPGVNSLFDIGSFQLLYFI 562  
Db 475 HSTGEYFRVTGETLSVLGLYFFFGIQ-YFVQRRPSLTKLIVDSYSEVLFFVHSLULLS 533  
QY 563 SAALYLAGIEAYLVAVFALVGLWGNALYFTRGLKLTGYSTMIQILFKDLFRFLVYL 622  
Db 534 SVLYFCGQELYVAVSMVFSALGWNALYTRGFQMGYISVNIAMILRDLRCRFMAYL 593  
QY 623 LEWIGYASALVSLNCPANMKVCNEDQ-TNCTVPTPCSRDSETFST-----FLDLF 674  
Db 594 VFLGTFSTAVTILIED-----DNEGQDTNSS--EYARSHTKRGFTSYNSLYTLELF 645  
QY 675 KLTIGMDLEMLSTKYPVVFIILVYIILTFVLLNMLIALMGETVGVQVSKESKIHWK 734  
Db 646 KFTIGMDLEFTENYRFSKVFVILLVYIILTFVLLNMLIALMGETVGVQVSKESKIHWK 705  
QY 735 LQWATTILDIERSFPVFLKAFRSGEMVTYVCKSDGTDPDRRCFRVDEVNWSHWNQNLGII 794  
Db 706 LQWATTILDIERSFPVFLKAFRSGEMVTYVCKSDGTDPDRRCFRVDEVNWSHWNQNLGII 765  
QY 795 INEDPG-----KNETYQYVGFSGHTVGLRRDRWSVPRVVELNKNNSPDEVVPLDSMGNPCDGG 841  
Db 766 INEDPGCSGDLARNPSY-----CIKPGRVSGKNMKTLPVLLRDSRRRETPKLPPEI 817

RESULT 13  
Q9JM57 PRELIMINARY: PRT: 838 AA.  
AC Q9JM57;  
DT 01-OCT-2000 (TremBLrel. 15, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TremBLrel. 21, Last annotation update)  
DE Vanilloid receptor type 1 like protein 1.  
GN VR1L1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tsutsumi S., Nakamura A., Kohama K.;  
RT "Vanilloid receptor type 1 like protein 1."  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB040873; BAA94307.1; -.  
DR InterPro; IPR002110; ANK.  
DR InterPro; IPR000636; Cat\_channel\_trpL.  
DR InterPro; IPR004729; Trp\_Cachannel.  
DR Pfam; PF00023; ank; 3.  
DR Pfam; PF00520; Ion\_trans; 1.  
DR SMART; SM00248; ANK; 3.  
DR TIGRFAMs; TIGR00870; trp; 1.  
DR PROSITE; PS50088; ANK\_REPEAT; 1.  
DR PROSITE; PS50297; ANK\_REPEAT; 1.  
KW ANK repeat; Receptor; Repeat.

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SO SEQUENCE 838 AA; 94964 MW; EE33CE4A606C3404 CRC64;

Query Match 39.7%; Score 1819; DB 11; Length 838;
Best Local Similarity 50.8%; Pred. No. 1.3e-132;
Matches 363; Conservative 133; Mismatches 187; Indels 32; Gaps 11;

QY 130 KQPSKAPAPQPPILKVFNRPIIDFIVSRGSTADLGLPFLTHKKRLTDEEREPS 189
DB 95 ROSQDSVSAGEKPP--RLYDRSIFDAVAQSCQELSLPFLQSKRLTDEEREPS 152
QY 190 TGKTCPLKALLNLSNGRNDIPVLLDIAERTGNMREFINSPFRDIYRGOTAHIAIER 249
DB 153 TGKTCPLKALLNLSNGRNDIPVLLDIAERTGNMREFINSPFRDIYRGOTAHIAIER 212
QY 250 CKHYVELLVQAQADVAHQARGFQPKDEGGYFYGELPLSLAACNQPHIVNLYTENPH 309
DB 213 NMTLVTLVLLVNGADVQAANGDFKTKRGPRGYFGEPLSLAACNQIAVFLQLNSW 272
QY 310 KKADMRDROSGNTVHALVAIADNTRENTKFTVMYDILLKLCARLPDSNLEAVLNND 369
DB 273 OPADISARDSVGNVTALHALVEADVADNTVDNFKVTSWNEILILGAKLHPTLKEEITNRK 332
QY 370 GLSPLMAAKTGIGIFQHIIIRREVTDDETRHLSRKFQKWAYGVPVYSSLYDLSSDTCGE 429
DB 333 GLTPLALAASSGKIGVLAYILOREIHEPECHLSRKFTWAYGVPVHSSLYDLSCIDTC-E 391
QY 430 EASVLEILVY-NSKIENRHEMLAVEPINELLRDKWRKFGAVSYINVSVLCAMVFTLT 488
DB 392 KNSVLEIVAYSSETPNRHDMLLVEPLNRLLOQKWDKRFVKRIEYFNFFVYCLYMIIFTAA 451
QY 489 AYYOPELEGTPPYRTV-DYLRAGEVITLFGVLFFFTNINIKDLFWKCPGNSLFDIG 547
DB 452 AYYRPELEGTPPYRTV-DYLRAGEVITLFGVLFFFTNINIKDLFWKCPGNSLFDIG 510
QY 548 SFOLLFYISVLVIVSAALYLAGIEAYLVAMVVLGWMNLYFTRGKLTCTYSIMIQ 607
DB 511 YSILEFVOSLFLVSVLYFSORKEYVASWFSPLANGWNTNMLYTRGFQMGYIYAVMIE 570
QY 608 KILFKDLFLVLLYLFMIGYASALVSLNPNCAKMKVCNEDQNTCTVP---TYPSCRDS- 663
DB 571 KMLRDLRFMFVYLVFLFGFSTAVVTLI-----EDGKNNSLPWESTPHKCRGSA 620
QY 664 -----ETFSFLDLFLKLTICMGDLEMSLTKYVPVFIILLYIITLTVLLNMLI 715
DB 621 CKPGNSYNSLYST-CLELFKFTIGMGDLFTENYDFKAVFIILLYIITLTVLLNMLI 679
QY 716 ALMGETVGVSKESKHIWKLQWATTILDIERSPVFLRKAFRSGEMVTYKSSDGTGDDR 775
DB 680 ALMGETVGVSKESKHIWKLQWATTILDIERSPVFLRKAFRSGEMVTYKSSDGTGDDR 739
QY 776 WCFRDEVNWNHQNGLIENEDPGKNE-TYQYGFSTVGRURDRWS--SVYP 827
DB 740 WCFRDEVNWNHQNGLIENEDPGKNE-TYQYGFSTVGRURDRWS--SVYP 794

RESULT 14
O35433 PRELIMINARY; PRY; 838 AA.
AC O35433;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vanilloid receptor subtype 1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98007969; PubMed=9349813;
RA Caterina M.J., Schumacher M.A., Tominaga M., Rosen T.A., Levine J.D.,
RA Julius D.,
RA "The capsaicin receptor: a heat-activated ion channel in the pain
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RT pathway";
RL Nature 389:816-824(1997).
DR EMBL; AF029310; AAC53398.1; -.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR000636; M+channel_nlg.
DR InterPro; IPR004729; Trp_Cachannel.
DR Pfam; PF00023; ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR SMART; SM00248; ANK; 3.
DR TIGRFAMs; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Receptor; Repeat.
SQ SEQUENCE 838 AA; 94947 MW; DAFC80B12BDF71BF CRC64;

Query Match 39.7%; Score 1818; DB 11; Length 838;
Best Local Similarity 45.6%; Pred. No. 1.5e-132;
Matches 388; Conservative 141; Mismatches 222; Indels 100; Gaps 18;

QY 16 AELPGDESOTPGGE-----AFPLSSLANLFEDEGSLSPSPADA 54
DB 5 ASLDSSESPPOENSCLDPPDRDPNCKPPPKPHIFTRSRTRLF-GRGDSEASPLDC 63
QY 55 SRPAGPGDGRPNLRMKFQAGFRKGVN-PIDLLLESTLYESSVVPKPKAPMDSLFYGT 113
DB 64 PYEEG-----GLASCPITIVSSVL-----TIORPGDG-----ASV 94
QY 114 RHSSDNKRWRKIIIEKQSPKAPAPQPPILKVFNRPIIDFIVSRGSTADLGLPFL 173
DB 95 RPSQDS-----VSAGEKPP--RLYDRSIFDAVAQSCQELSLPFL 136
QY 174 LTHKKRLTDEEREPSTGKTCPLKALLNLSNGRNDIPVLLDIAERTGNMREFINSPFR 233
DB 137 QRSKKRLTDEEREPSTGKTCPLKALLNLSNGRNDIPVLLDIAERTGNMREFINSPFR 196
QY 234 IYRGOTAHIAIERCKHYVELLVQAQADVAHQARGFQPKDEGGYFYGELPLSLAA 293
DB 197 SYKGTALHIAIERNTLVTLVLLVNGADVQAANGDFKTKRGPRGYFGEPLSLAA 256
QY 294 CTNQHIVNLTENPHKADMRDROSGNTVHALVAIADNTRENTKFTVMYDILLKLC 353
DB 257 CTNQLAIVFLLNSQWOPADISARDSVGNVTALHALVEADVADNTVDNFKVTSWNE 316
QY 354 ARLPDSNLEAVLNNDGLSPLMAAKTGIGIFQHIIIRREVTDDETRHLSRKFQKWAYG 413
DB 317 AKLHPTLKLEETINRKGTLPLALAASSGKIGVLAYILOREIHEPECHLSRKFTWAYG 376
QY 414 VYSSLYDLSSDTCGEASVLEILVY-NSKIENRHEMLAVEPINELLRDKWRKFGAVSY 472
DB 377 VHSSLYDLSCIDTC-EKNSVLEIVAYSSETPNRHDMLLVEPLNRLLOQKWDKRFVKRI 435
QY 473 INVSVLCAMVFTTAYTQPEGTPPYRTV-DYLRAGEVITLFGVLFFFTNINIKD 531
DB 436 FNEFVYCLYMIIFTAAAYRPELEGTPPYRTV-DYLRAGEVITLFGVLFFFTNINIKD 494
QY 532 LEWKCPGNSLFDIGSPOLLFYISVLVIVSAALYLAGIEAYLVAMVVLGWMNLY 591
DB 495 YFLORRPSLKLFDVSYSEILFFVQSLFVLVSVLYFSORKEYVASWFSPLANGWNTN 554
QY 592 FTRGLKLTCTYSIMIQILFKDLFRLLYLLFMIGYASALVSLNPNCAKMKVCNEDQNT 651
DB 555 YTRGFQMGYIYAVMIEKMLRDLRFMFVYLVFLFGFSTAVVTLI-----EDGKN 604
QY 652 CTVP-----TFSFLDLFLKLTICMGDLEMSLTKYVPVFIIL 699
DB 605 NSLPWESTPHKCRGSAKCPGNSYNSLYST-CLELFKFTIGMGDLFTENYDFKAVFI 663
QY 700 VTYIITLTVLLNMLIALMGETVGVSKESKHIWKLQWATTILDIERSPVFLRKAFRSG 759
DB 664 LAYVILTYILLNMLIALMGETVGVSKESKHIWKLQWATTILDIERSPVFLRKAFRSG 723
QY 760 EMVTGKSSDGTGPDRCWCFRDEVNWNHQNGLIENEDPGKNE-TYQYGFSTVGRUR 818
```

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Db 724 KLLQVFTDGDYRCVDEVTNTWNTNNGIINEDPGNCEGVKRTLSFSLRSGRVS 783
QY 819 RDRWS--SVVP 827
Db 784 GRNKNFALVP 794

RESULT 15
Q9N074 PRELIMINARY; PRT; 839 AA.
AC Q9N074;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Vanilloid receptor 1.
GN VR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kelsell R.E.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=20504379; PubMed=11050376;
RA Hayes P., Meadows H.J., Gunthorpe M., Harries M.H., Duckworth M.D.,
RA Cairns W., Harrison D.C., Clarke C., Ellington K., Prinjha R.K.,
RA Barton A.J., Hedderley A.D., Smith G.D., Topp S., Murdock P.,
RA Sanger G.J., Terrett J., Jenkins O., Benham C.D., Randall A.D.,
RA Gloger I.S., Davis J.B.;
RT "Cloning and functional expression of a human orthologue of rat
RT vanilloid receptor-1";
RL Pain 88:205-215(2000).
DR EMBL; AJ277028; CAB95729.1; -.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR000636; M+channel_nlg.
DR InterPro; IPR004729; Trp-CaChannel.
DR Pfam; PF00023; ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR SMART; SM00248; ANK; 3.
DR TIGRfams; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Receptor; Repeat.
SQ SEQUENCE 839 AA; 94924 MW; 7142FEAE43189ECC CRC64;

Query Match 39.3%; Score 1800; DB 4; Length 839;
Best Local Similarity 44.9%; Pred. No. 3.9e-131;
Matches 374; Conservative. 156; Mismatches 222; Indels 81; Gaps 15;

QY 49 PSPADASRPAGDGRPNL-----RMKFGQ-----AFKRGVNPIDLES--TLYESV 95
Db 22 PDPLDGDNSRPPPAKPOLSTAKSTRFLGKGDSEAFVDCPHEEGELDSCPTITVSPV 81
QY 96 V-----PGPKAPMDSLFYGYTHHSSDNKRWKKTIKQOPQSPKAPAPOPPPILKVF 149
Db 82 ITIQRPDGTGARGL-----LSQDSVAASTEKTRLY 113
QY 150 NRPILFDIVSRGSTDLDGLLPFLTHKKRLTDEFEPSGTCTCLPKALLNSGRNDT 209
Db 114 DRRSIFEAVANNCDLESLLFLQKSKKHLLTNEFKDPTGKTCLLKAMLNLDGQNT 173
QY 210 IPLVDIAERTGNREFNSPRDIYRGQTALHAIERRCKHYVELLVAQADVHAQAR 269
Db 174 IPLLEIARQDLSKELYNASYDSYKQGTALHAIERNWALVTLVENCADVQAAAH 233
QY 270 -GRFPQKDEGGYFYFGEPLSLAACTNQPHVNTLTENPHKKADMRQDSRGNTVLHALV 329
Db 234 GDFKTKKGRGPFYFGEPLSLAACTNQLGIVKFLQNSWQTADISARDSVGNVTVLHALV 293
```

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QY 330 ATADNTRENTKFTKMYDILLKLCARLPDPSNLEAVLNNDGSLPLMAAKTKIGIFOHT 389
Db 294 EVADNTADNTKFTVSMYNEILLGAKLHPTLKEELTNKKGMTPLAAGTAKIGVLAT 353
QY 390 IRREVTDETRHLSRKFKDWAYGPVYSSLYSLSSLDTCGEASVLEILVY-NSKIENRHE 448
Db 354 LQREIQEPECRLSRKFTWAYGPVHSSLYDLSDICDTC-EKNSVLEVIAYSSSETPNRHD 412
QY 449 MLAVEPINELLRDKWRKFCVAFYINWVSYLCAWITFTTAYIQPLEGTPPYRTVDY 508
Db 413 MLVLEPLNRLQDKWDRFYKRFYFNFLVYCLYMIIFTMAAYRYPVDGLPPKMEKMGDY 472
QY 509 LRLAGEVITLFTGVLFFFFTNIDLPKMKCPGVNSLFDIGSFOLLXYFIYSVLTVSAALYL 568
Db 473 FRVTGEILSVLGVYFFFRGQIO-YFLQRRPSKMTLFDVDSYSEMLFQLQSLFMLATVVLIF 531
QY 569 AGIEAYLAVMVFALVGLGMNALLYTRGLKLTGTYSIMIQILFKDLFRELLVLLPFI 628
Db 532 SHLKEYVASMVFSLAGWTNMLYTRGFQOMGIYAVMIEKMLRDLCLRFMFVYVFLPGF 591
QY 629 ASALVSLNPNCANMKVCNEDQTNCTVPTY-----PSCRSET-----FSTFLDLDFK 675
Db 592 STAVVTLI-----EDGKNDSLPSSESTSHRWGPACRPPDSSYNSLYST-CLELEFK 640
QY 676 LTIGMDLEMLSSTKYPVVFIIILVTYIILTFVLLNMLIALMGETVGOVSKESKHIWKL 735
Db 641 FTIGMDLETFENYDFKAVFIILLAYVILTILLNMLIALMGETVKNKIAESKNWKL 700
QY 736 QWATTILDIERSFPVFLRKAFKRGEMVTVGKSSDGTDRRMCFRVDEVNWSHWNQNLGII 795
Db 701 QRAITILDTEKSFSLKCMRKAFKSGKLLQVYTPDGKDDYRMCFRDEVNWTWNTNNGII 760
QY 796 NEDPGKNE-TYQYGFSGHTVGLRRDRWS--SWVPRVVELN-----KNSNPDEV 841
Db 761 NEDPGNCEGVKRTLSFSLRSGRVRGHWKMFALVPLLRASARDRQSAQPEEV 813
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Search completed: June 3, 2003, 19:55:32

Job time : 49 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 3, 2003, 19:52:38 ; Search time 26. Seconds  
(without alignments)  
3216.806 Million cell updates/sec

Title: US-09-870-090A-2

Perfect score: 4577

Sequence: 1 MADSSSEPRAGPGEVAELPG.....PRCDGHQGGYPRKWRDAP 870

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1818	39.7	838	2 T09054	capsaicin receptor
2	1795	39.2	839	2 JC7621	capsaicin receptor
3	764.5	16.7	727	2 JC7796	epithelial calcium
4	757	16.5	723	2 JC7795	epithelial calcium
5	753.5	16.5	725	2 JC7531	calcium transport
6	503.5	11.0	937	2 T37241	olfactory channel
7	503.5	11.0	957	2 D8651	protein R0212.5 [1
8	445	9.7	900	2 T33026	hypothetical prote
9	342.5	7.5	790	2 T20312	hypothetical prote
10	278	6.1	519	2 T24772	hypothetical prote
11	235.5	5.1	1188	2 T19552	hypothetical prote
12	188	4.1	828	2 JC5807	trp3 protein - rat
13	148	3.2	1124	2 JH0588	calmodulin-binding
14	138.5	3.0	810	2 I38361	TRAP1 protein - hu
15	138	3.0	616	2 T00894	hypothetical prote
16	137	3.0	1765	2 T42388	sodium channel alp
17	136.5	3.0	683	2 A85044	hypothetical prote
18	136	3.0	2352	2 T30201	Notch homolog prot
19	134	2.9	481	2 T23729	hypothetical prote
20	134	2.9	1275	2 J00092	trp protein - fru
21	132	2.9	1274	2 J00015	trp protein - fru
22	131.5	2.9	642	2 S58154	hypothetical prote
23	130.5	2.9	652	2 D85044	hypothetical prote
24	129.5	2.8	608	2 G02640	polycystic kidney
25	129	2.8	823	2 S44873	IC21.2 protein - C
26	127.5	2.8	643	2 D86167	protein F21B7.27 [
27	127.5	2.8	4377	2 A55575	ankyrin 3, long sp
28	126.5	2.8	2471	2 A49128	cell-fate determin
29	125.5	2.7	934	1 H71274	probable ankyrin -

30 125.5 2.7 2529 2 B64635 toxin-like outer m  
31 125 2.7 1957 2 S68453 sodium channel pro  
32 124 2.7 793 2 S68238 trp-1 protein - hu  
33 123.5 2.7 968 2 A37867 transcription fact  
34 123 2.7 751 2 F85043 hypothetical prote  
35 123 2.7 2212 2 A41098 calcium channel pr  
36 123 2.7 2531 2 T31070 notch homolog - se  
37 121 2.6 1549 2 T13940 ankyrin - fruit fl  
38 120.5 2.6 397 2 T46445 hypothetical prote  
39 120.5 2.8 573 2 D86464 F12G12.13 protein  
40 120.5 2.6 638 2 A56695 notch2 protein hom  
41 120 2.6 633 2 T27499 hypothetical prote  
42 119.5 2.6 574 2 T47566 hypothetical prote  
43 119.5 2.6 2108 2 S72458 sodium channel pro  
44 119 2.6 1765 2 T42714 ankyrin 3, splice  
45 119 2.6 1940 2 T42715 ankyrin 3, splice

RESULT 1  
T09054  
capsaicin receptor - rat  
N:Alternate names: vanilloid receptor subtype 1  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C:Accession: T09054  
R:Caterina, M.J.; Schumacher, M.A.; Tomimaga, M.; Rosen, T.A.; Levine, J.D.; Juli  
Nature 389, 816-824, 1997  
A:Title: The capsaicin receptor: A heat-activated ion channel in the pain pathway,  
A:Reference number: Z16539; MUID:98007969; PMID:9349813  
A:Accession: T09054  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-838 <CAT>  
A:Cross-references: EMBL:AF029310; NID:g2570932; PIDN:AAC53398.1; PID:g2570933  
A:Experimental source: dorsal root ganglion  
C:Keywords: ion channel; receptor

#### ALIGNMENTS

Query Match 39.7% Score 1818; DB 2; Length 838;  
Best Local Similarity 45.6%; Pred. No. 1e-123;  
Matches 388; Conservative 141; Mismatches 222; Indels 100; Gaps 18;

Qy 16 AELPGDEGCPGGE-----APFLSSLANLPEGEDGSLSPSPADA 54  
Db 5 ASDSESESPPOENSCLDPPDRDCKPPVPKPHFTTRSRRLF-GKGDSEASPLDC 63  
Qy 55 SRPAGPGDGRPNLRMKFQGAFRKGVNP-PIDLLLESTLYESSVVPKPKAPMDSLFYDGY 113  
Db 64 PYEEG-----GLASCPITVSSVL---TIQPCDGP-----ASV 94  
Qy 114 RHSSDNKRWRKIIIEKQPOSKAPAPPPPIIKVNRPIFDIVSRGSTADLGLLPFL 173  
Db 95 RPSQDS-----VSAGEKPP--RLYDRRSIFDAVQAQNCQEELESLLPFL 136  
Qy 174 LTHKRLTDEEFREPSTGKTCPLKALLNSGNRNDITPVLLDTAERTGNMREFINSFPRD 233  
Db 137 QRSKRLTDEFEKDPETGKTCCLKAMLNHNGNDITALLDVARKTDSUKQFVNASITD 196  
Qy 234 IYRGOTALTHAIATERCKHYVELLVAGQADHVAQAGRRFFQKDEGGYFFYFGEPLSLAA 293  
Db 197 SYKGGTALTHAIATERNMVTLVLLVENGADVQAAGDFPKTKGRPGFFYFGEPLSLAA 256  
Qy 294 CTNQHIVNYLTENPHKKADMRQDSRGNTVLHALVAIDNTRENTKFTVKMYDLLLLKC 353  
Db 257 CTNQLATVRFLLQNSQPADISARDSVGNVTLHALVEADVNTDNTKFTVSMYNEILIG 316  
Qy 354 ARLPDSNLEAVLNQGLSPLMAAKTGKIGIQHIIIRREVTDTRHLSRKRKDWAYGP 413  
Db 317 AKLHPTKLKEITNRKGLTPLAASGSGKIGVLAYILQREIHEPECRHLSRKRFTWAYGP 376  
Qy 414 VYSSLDLSLSDTCGEASVLEILVY-NSKIENRHEMLAVEPINELLRDKWRKFGAVSFY 472

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Db      377 VHSYLDUSCIDTC-EKNSVLEIVAYSSETPNRDMMLVLEPLNRLLODKWDRFVKRIFY 435
Qy      473 INVSYLCAMIFITLTAIYQLEGTPPYRYTIV-DYLRLAGEVITLFTGVLFETNIKO 531
Db      436 ENFVYCLYMIIFIAAAYRPEGLPPYKLNKNTVDYFRVTEILSVSGVYFFERGIO- 494
Qy      532 LFMKKCPGVNSLFDIGSQQLYFIYSLVIVSAALYLAGIAYLAVWVVALVGLWMMNLY 591
Db      495 YFLORPRLSKLFLVDVSEILFFVQSLFVSVVLYFSQRKEYVASVMVFLSANGWNTNLY 554
Qy      592 FTRGLKLTGTYSIMOKILFKDLFRFLVYLLEFMIGVASALVSLNPPCANMKVCNEDOTN 651
Db      555 YTRGFOQGIYAVMIERKMLRDLCLRFMFVYLVLFGEFSTAVVTII-----EDGKN 604
Qy      652 CTVP---TYPSCRS-----ETFTFLDLFLKLTIGMDLEMLSLSTKYVPVFIILL 699
Db      605 NSLPWESTPHKCRGSACKPGNSYLSYST-CLELFKFTIGMDLEFTEYDFKAVFIILL 663
Qy      700 VTYILFVLLNMLIALMGTEVGOVSKESKHIWKLQWATWITLIDERSFPVFLKAPRSG 759
Db      664 LAYVILTIVILLNMLIALMGTEVANKIAQESKNIWKLQRAITLIDTEKSFCKMRKAPRSG 723
Qy      760 EMVTVGKSSDCTPDRRCFRVDEYNWASHNQNGLIINEDPGKNE-TYQYGFSTVTVGLR 818
Db      724 KLLQVGFTPDGKDDYRCVDEVNTWNTNNGIINEDPGNCGEVKRTLSFSLRSGKVS 783
Qy      819 RDRWS--SWVP 827
Db      784 GRNKNKALVP 794

RESULT 2
JC7621
A:Species: Homo sapiens (man)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7621
R:Corrington, D.N.; Crandall, M.; Sanchez, J.F.; Zou, T.; Krause, J.E.; White, G.
Biochem. Biophys. Res. Commun. 281, 1183-1189, 2001
A:Title: The tissue distribution and functional characterization of human VR1.
A:Reference number: JC7621; MUID:21139751; PMID:11243859
A:Contents: Dorsal root ganglia
A:Accession: JC7621
A:Molecule type: mRNA
A:Residues: 1-839 <COR>
A:Cross-references: GB:AF196175
C:Comment: This receptor, a transmembrane protein with many phosphorylation sites, is a
its integrative activation by several noxious stimuli, and plays an important role in In
C:Genetics:
A:Gene: vrl
A:Map position: 17p13
C:Keywords: transmembrane protein
F:201-233/Domain: ankyrin #status predicted <ANK1>
F:248-280/Domain: ankyrin #status predicted <ANK2>
F:333-385/Domain: ankyrin #status predicted <ANK3>
F:433-455/Domain: transmembrane #status predicted <TM1>
F:477-495/Domain: transmembrane #status predicted <TM2>
F:508-531/Domain: transmembrane #status predicted <TM3>
F:543-569/Domain: transmembrane #status predicted <TM4>
F:578-597/Domain: transmembrane #status predicted <TM5>
F:624-644/Region: pore loop #status predicted
F:656-684/Domain: transmembrane #status predicted <TM6>

Query Match          39.2%; Score 1795; DB 2; Length 839;
Best Local Similarity 44.8%; Pred. No. 4.9e-122;
Matches 373; Conserved 156; Mismatches 223; Indels 81; Gaps 15;

Qy      49 PSPADSRAPGPGGRPNL-----RMKFQ-----AFRKGVPNPIDLLS--TLYESSV 95
Db      22 PDPLDGPNSRPPPAKPOLSTAKSRTRLFKGGDSEAFVDPDCEHEGELDSCTITVSPV 81
Qy      96 V-----PGPKAPMDSLSFDYGYRHHSSDNKRKRKIIIEKQPQSRAPAPQPPILKVF 149
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Db      82 ITIQRPDGPCTCARL-----LSQDSVAASASTKTLURLY 113
Qy      150 NRPTLFDVSGSTADLDGLPFLTHKKRLTDEEFPSTGKTKLKPALLNLNGRNDT 209
Db      114 DRSIFPAVAQNQCODLESLLFLQSKKHLTDNEFKDPETGKTKCLLKAMNLHDGQNTT 173
Qy      210 IPVLLDIAERTGNMREFINSFPRDIYRGQTALHAIERRKHYVELLVVAGADVHAQAR 269
Db      174 IPLLEIARQTDLSKELVNASYTSYKGGTALHAIERRNMAVLTLLVENGADVQAAAH 233
Qy      270 GRFPQKDEGGYFFGELPLSLAQTNPQTHVNVLTENPHKKADMRQDSRGNTVHALY 329
Db      234 GDFPKTKGRGFYFGEPLSLAQTNPQTHVNVLTENPHKKADMRQDSRGNTVHALY 293
Qy      330 AIAONTRENTKFTVMYDMLLLKCARLPDPSNLEAVLNNDGLSLPLMAAKTKGKIGFOHI 389
Db      294 EVAONTADNTKFTVMYNEILMLGAKLHPTLKLEELNKKGMTPLAAGTKGLGVLAYI 353
Qy      390 IRREVTDDETRHLSRKFKDMAYGPVSYSLYDLSSLDTCGEASVLEILVY-NSKIENRHE 448
Db      354 LQREIQPECRHLSRKFTENAYGPVSHSLYDLSDICDTC-EKNSVLEIVAYSSETPNRHD 412
Qy      449 MLAVEPINELLROKWRKFGAVSYFVNVVSYLCAMVITLTAIYTOPLEGTPPYRYTVDY 508
Db      413 MLLVEPLNRLLODKWDRFVKRIFYFNFVLYCLYMIIFTMAAYRPVDGLPFPFKMEKIGDY 472
Qy      509 LRLAGEVITLFTGVLFETNIKDLFMKKKCPGVNSLFDIGSQQLYFIYSLVIVSAALYL 568
Db      473 FRVTEILSVLGGVYFFERGIO-YFLORRPSMKTLFVDSYSEMLFFLOSLFMLATVVLXF 531
Qy      569 AGIEAYLAVWVVALVGLWMMNLYTRGLKLTGYYSIMQILFKDLFRFLVLLVLFMIGY 628
Db      532 SHLKEYVASVMVFLSALGWTNMLYTRGFQMGYVAVMIERKMLRDLCLRFMFVYLVLFGE 591
Qy      629 ASALVSLNPPCANMKVCNEDOTNCTVPTY-----PSCRDSET-----FSIFLDDLFX 675
Db      592 STAVVTII-----EDGKNSLPSSTSHRWGPACRPDPDSSVNSLYST-CLELFK 640
Qy      676 LTIGMGDLEMLSLSTKYVPVFIILLVYIITFVLLNMLIALMGTEVGOVSKESKHIWKL 735
Db      641 FTIGMGDLEFTEYDFKAVFIILLVAVIYLLNMLIALMGTEVANKIAQESKNIWKL 700
Qy      736 QWATTLIDERSFPVFLKAPRSGEMVTYVCKSDGTPDRRCFRVDEYNWASHNQNGLII 795
Db      701 QRAITLIDTEKSFCKMRKAPRSGKLLQVGTYPDGKDDYRCVDEVNTWNTNNGVYII 760
Qy      796 NEDPGKNE-TYQYGFSTVTVGLRDRWS--SVVPRVVELN---KNSNPDEV 841
Db      761 NEDPGNCGEVKRTLSFSLRSRVSGRHWKNFALVPLLRASARDRSQAQPEEV 813

RESULT 3
JC7796
epithelial calcium channel 2, ECac2 - mouse
N:Alternate names: Calcium T1; Cat1
C:Species: Mus musculus (house mouse)
C:Date: 02-Apr-2002 #sequence_revision 17-May-2002 #text_change 02-Apr-2002
C:Accession: JC7796
R:Weber, K.; Erben, R.G.; Rump, A.; Adamski, J.
Biochem. Biophys. Res. Commun. 289, 1287-1294, 2001
A:Title: Gene structure and regulation of the murine epithelial calcium channels E
A:Reference number: JC7796
A:Molecule type: DNA
A:Residues: 1-727 <WEB>
A:Cross-references: GB:AF336378
C:Comment: This calcium channel plays an important role in active transcellular ca
relevant for in vivo calcium homeostasis.
C:Genetics:
A:Gene: ECac2
A:Map position: 6
A:Introns: 43/2; 76/1; 117/1; 163/1; 196/1; 253/3; 302/3; 373/3; 402/3; 428/2; 483
```



C:Genetics:  
A:Gene: Cat1  
A:Map position: 7q33-34  
C:Keywords: calcium channel; calcium transport; intestine; kidney; transmembrane protein

Query Match 16.5%; Score 753.5; DB 2; Length 725;  
Best Local Similarity 31.9%; Pred. No. 1.7e-46;  
Matches 217; Conservative 106; Mismatches 250; Indels 107; Gaps 24;

QY 171 PELLTHK-----KRLDEFR---EPSTGKTCPLKALL--NLSNGRNDIPVLLDIA 217  
DB 48 PLLAAKNDVOALNKLKYEDCKVHHRGAMGATALHIAALYDNL-----EAAMLMEEA 102  
QY 218 ERTGNMREPFNSPFRDIYRGOTATLHIAIERCKHYVELLVAAGDVAHQARGRFQPKD 277  
DB 103 P-----ELVFPMTSYEGOTATLHIAVYVNMNMLVALLARRASVSARATGTAFR-RS 155  
QY 278 EGGYFYGGLPLSLAACTNQPHVNYLTENPHKKADMRQDSRGNTVHLHALVAIADNTR 337  
DB 156 PCNLIVFGHPLSFAACVNSEIVRLIEH---GADIRAQDSLGNTVLHLI-----LQP 207  
QY 338 NTKFTVMKYDLLLLKCARLPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTD 397  
DB 208 NKTFAOCYNLLSYDRHGDHLQPLDLVPHOGLTPFKLAGVEGNTVMFQHLMOQ----- 262  
QY 398 DTRHLRSRKFQWAYGPVYSSLYDLSLDTGCEASVLEILVYNSKIENRHEMLAVEPINE 457  
DB 263 -----RKHTQWYGLTSTLYDLTEIDSSGDEQSLELIITTKREAR-QILDQTPVKE 315  
QY 458 LLRDKWRKFGVSVFVNVVSYLCAMVIFTLTAYQPLE-----GTTP-----Y 500  
DB 316 LVSLAKWKRGPRYFCMLGAIYLYIICFTMCCYIYRPLKPTNNRTPSPRNDTLLOKLLQE 375  
QY 501 PYRTVDYLRAGEVITLFTGVLFVFTTKIDLFMKKCPGVNSLF-----IDGSFOLLYFIY 556  
DB 376 AYMTPKDDIRVLGELVTIGAIILLVEVPOIFRM---GVTRFQQTILGGPFPHLIITY 432  
QY 557 SVLVTVSAALYLAGIEAYLAVMVFAVLGWMNALYFTRGKLTGTYSIMIOKILFKDLFR 616  
DB 433 AFVWLVTWMLISASGEVPMSPFALVGLGWNVMTFARGFQMLGPTTMIOMKIFGDLMR 492  
QY 617 FLLVYLLPMIGYASALVSLNPNCAVMKVCNEDQTNCTVPTYPSCRDSETFSTLDDLFK 675  
DB 493 FCWLMAVYILGFASAFYIFQ-----TEDPELGHFYDYPMA---LSTF--ELF- 537  
QY 676 LTIGMDLEMLSSKYPVVFILLVYIILFTVLLNMLIALMGTVGQVSKESKHIWKL 735  
DB 538 LTIIDGPANY--NVDLPFMSITYAAFAIATLMLNLLIAMMGDTHRWVAHERDELWRA 595  
QY 736 QWATTILDIERSFPVFLRKAFRSGBMVTVGKSSDGTDRRCFCFRVDEVNHNQNLGII 795  
DB 596 QIVATVMLERKLPCLMP--RSG-----ICGREYGLGD--RWFLRVED----- 635  
QY 796 NEDPGKNETYQYGFSTVVG 815  
DB 636 QDLNLRQRIQRYAQAFHFRG 655

RESULT 6  
T37241  
olfactory channel protein osm-9 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000  
C:Accession: T37241  
R:Colbert, H.A.; Smith, T.L.; Bargmann, C.I.  
J. Neurosci. 17, 8259-8269, 1997  
A:Title: OSM-9, A novel protein with structural similarity to channels, is required for  
A:Reference number: 221639; MUID:97477445; PMID:9334401  
A:Accession: T37241  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-937 <COL>  
A:Cross-references: EMBL:AF031408; NID:g2642589; PIDN:AAB87064.1; PID:g2642590

C:Genetics:  
A:Gene: Osm-9  
A:Map position: IV  
C:Keywords: transmembrane protein

Query Match 11.0%; Score 503.5; DB 2; Length 937;  
Best Local Similarity 25.5%; Pred. No. 3.5e-28;  
Matches 171; Conservative 109; Mismatches 260; Indels 131; Gaps 22;

QY 233 DIYR-----GOTALHIAIERCKHYVELLVAAGDVAHQARGRFQPK-----DEG 279  
DB 163 DIYLGDEQFGGALHIAIVHDDYETVSLLSKADVNARACGNFFLPEDFKLTNKTIDYQ 222  
QY 280 GYFYEGELPLSLAACTNQPHVNYLTYE---NPHKKADMRQDSRGNTVHLHALVAIADNTR 336  
DB 223 GYAYGEYPLAFAACFGNKDIYDLILQGANPN-----LQDSFGNTILHMCV----- 269  
QY 337 ENTKEVTKMYDLLLLKCARLPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTD 396  
DB 270 --INTSSMYSYAVRHAK--PAD--PHVNHAGFTPLTKLGRKQIFEMLE----- 318  
QY 397 EDTRHLRSRKFQWAYGPVYSSLYDLSLDTGCEASV---LEILVYNSKIENRHEMLAV 452  
DB 319 -----INKVEFRFSDMTCSAYPLNTLDTIQDGSNTYDSALMTVINGSTPEHLDMLGS 372  
QY 453 EPINELLRDKWRKFGVSVFVNVVSYLCAMVIFTLTAYQPLEGTPPYPTTV---DYL 509  
DB 373 EVIQRLLADKWKAFQAKRLIERLVLLIVQLITLSIVVYIRPTE--LPRLYMEDPQWDDYI 430  
QY 510 RLAGVITLFTGVLF-----FFTNKIDLFMKKCPGVNSLFDGFSFOLLY 553  
DB 431 RTACELLTILNCIIFVGVQGLQETRTQGMRYLRNLKTPAKAVFCIANLFL----- 482  
QY 554 FYSVLVTVSAALYLAGIEAYLAVMVFAVLGWMNALYFTRGKLTGTYSIMIOKILFKD 613  
DB 483 ---LLCIPFRLLMKKHEIEE--ALFVPALPQSNIFLFFARSAKLTGPFVQMIYSMIAGD 536  
QY 614 LFRLLVYLLPMIGYASALVSL--LNPCANMKVCNEDQTNCTVPTYPSCRDSETFSS 667  
DB 537 MIRFAITSAIFLVFSQVYFVGVKMDAKOKLEDTPHACRISGYTIYV-----NTFP 590  
QY 668 TFLDLRLKLTIGMDLEMLSSKYPVVFILLVYIILFTVLLNMLIALMGTVGQVSK 727  
DB 591 EFTTLFRASGGDYDEFFSCANYQALTKTLFLVYMFVMPIMINILIAMMGNTYTTVIA 650  
QY 728 ESKHIWLOWATTILDIERSFPVFLRKAFRSGEMVTVGKSSDGTDRRCFCFRVDEVNHN 787  
DB 651 QAERARQOYQAIVMWLERS-----VCKERLAASOLEYSIRLQDEGSSG 694  
QY 788 WN--ONLGIINDEPKNETYQYGFSTVVGRLRRD---RWSSVYPRVVELNKNKSNPDEVV 843  
DB 695 MEVRGLMVIKQT-----KKTRARQOKAIYNWKTIGRKVIHTIDKVGTEQAVL 742  
QY 844 PLDSMGNPRCD 854  
DB 743 LLH--GHRDL 751

RESULT 7  
D88651  
protein B0212.5 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C:Accession: D88651  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating  
A:Reference number: A75000; MUID:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/projects  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 195  
A:Accession: D88651  
A:Status: preliminary  
A:Molecule type: DNA

A;Residues: 1-957 <STO>  
A;Cross-references: GB:chr\_IV; PIDN:AAO2569.1; PID:g2854148; GSPDB:GN00022; CESP:B0212  
A;Note: contains similarity to ankyrin repeats  
C;Genetics:  
A;Gene: B0212.5  
A;Map position: 4

Query Match	11.0%	Score	503.5	DB	2	Length	957
Best Local Similarity	25.5%	Pred. No.	3.6e-28				
Matches	171	Conservative	109	Mismatches	260	Indels	131
Gaps	22						
Qy	233	DIYR	---	COTALHTAIERCKHYVELLVAQADVHAQARGRFQPK	-----	DEG	279
Db	166	DIYGLBQFGQSALHAIHDDVETVSLLSKADVARNACGNFFLPEDFKLNKIDYQ	225				
Qy	280	GYEYFGEPLSLAACTNQPHIVNLT	---	NPHKADMRQDSRGNTVHLHALVAIADNTR	336		
Db	226	GYAYGEYPLAFACGKNKIYDLITQGANPN	-----	LQDSFGNTILHMCV	-----	272	
Qy	337	ENTKFTVKHYDLLLLKCARLPDSNLLEAVLNNDGLSLPMAAKTKIGIFQHIIRREVD	396				
Db	273	--INYSMSYSAVRHWAK	--PAD--	PHVNHAGFTPLTLATLGRKQIEEMLE	-----	321	
Qy	397	EDTRHLSRPFKNWAYGPVYSSLYDLSLDTGCEASV	---	LEILYNSKIEHNHEMLAV	452		
Db	322	-----IMKVEFWFRFSDMTC	SAYPLNTLDTIQDGSNTYDSALMTVINGSTPEHLDMIGS	375			
Qy	453	EPINELLRDKWRKFGAVSFYINVVYSLCAMVITLTAYOPLGTPPYRYRTTV	---	DYL	509		
Db	376	EVTORLLADKKWAKFAOR	KLIERLVLLIVQILITISVIVYIRPTE	--LPRLYMEDPQWDDYI	433		
Qy	510	RLAGEVITLTGTGLVLF	-----	FFTNIKDLFMKPCGNSLFDIGSFOLLY	553		
Db	434	RTACELLTILNCIFFVGYQOLGEIRTOGMRGYLRNLK	TAPAKAVFCIANFL	-----	485		
Qy	554	FYISVLVIVSAALYLAGIEAYLAWVWFALVGLGMNALYFTRGKLKLTGTSIMQKILFKD	613				
Db	486	-----LLCIPFLRMKKHEIEE	--ALFVFALPGSWIFLLFFARSAKLTGPVQMTYSIAGD	539			
Qy	614	LFRFLVYLLFMIGYASALVSL	--LNP	CANKVCNEDQTN	-----	RVPTYPSCRDSFTFS	667
Db	540	MIRFAISALFLVSFQVYFVYFGKMDAKQKLEDTPHACRISGYIITY	-----	NTFP	593		
Qy	668	TELLDLFKUTIGNGDLEMISSTKYPVFIILLVYIILFTVLLNMLIALMGTEGVQVSK	727				
Db	594	ETFITLFRASMGYDYEEFSCANYQALTKTLFVLYMFVMP	IMMINILIAMMGNITYTIVA	653			
Qy	728	ESKHIWKLOWATITLLDIERSPFVFLRKARFSGEWTVGKSSDCTPDRRCFRVDEVNWSH	787				
Db	654	QAEKAWROQYAOIVMWLERS	-----	VGKERLAASOLEYSIRLDQEGSSG	697		
Qy	788	WN--QNLGIIINEDPGKNETYYCYGFSHTVGRLRD	---	RWSSVVVPVVELNKNKNSPDEVVV	843		
Db	698	MEVRGLMWIKQT	-----	KKTRARQKQAIYNHKTGRKVIHIDKVGTEQAVL	745		
Qy	844	PLDSMGNPRCD	854				
Db	746	LLH--GHDRLD	754				

RESULT 8  
T33026  
hypothetical protein T09A12.3 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C:Accession: T33026  
R:Hawkins, J.; Fulton, B.; Gillam, B.  
submitted to the EMBL Data Library, February 1998  
A:Description: The sequence of C. elegans cosmid T09A12.  
A:Reference number: Z1265  
A:Accession: T33026  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA

A: Residues: 1-900 <HAW>  
A: Cross-references: EMBL:AF047660; PIDN:AC04431.1; GSPDB:GN00022; CESP:T09A12.3  
A: Experimental source: strain Bristol N2; clone T09A12  
C: Genetics:  
A: Gene: CESP:T09A12.3  
A: Map position: 4  
A: Introns: 43/2; 86/3; 260/2; 396/3; 424/2; 495/1; 517/3; 553/3; 691/3; 741/3; 781/3

Query Match	9.7%	Score 445;	DB 2;	Length 900;
Best Local Similarity	24.8%	Pred. No. 5.8e-24;		
Matches 181;	Conservative 104;	Mismatches 250;	Indels 194;	Gaps 29;
Qy	189	STGKTCLPKALLNLNSGRNDTIPVLDDIAERTGNMREFINSFPERDIY-----YRGOTPALHI 244		
Db	154	SMGETICCLLHASDIINALVKILDYYPKLLN-----DIHISEDYGLSPLHQ 203		
Qy	245	A-IERRCKHYVELLVAQADYHAQAGRRFFQPKDE-----GGYF 282		
Db	204	AIINTDCK-LVYKFLKGADVNSRCYGAFFCADDQKASRTDSLEHEYVELSLKTYNTGNM 262		
Qy	283	YFGELPLSLAECTNQPHVINYLTENPHKKADMRRODSRGNTVLHALVAIADNTRENTKVF 342		
Db	263	YLGEYPLSFAACLNOPEFRULLA---FKANPAQDTNGNSVLHMCV-----IHENMAFM 314		
Qy	343	TKMYDLLLKKCARLFPDSNLEAVLNNDGLSPLMAAQTGKIGIFQHIIRREYTDDETRHL 402		
Db	315	K-----LALECG-----ASLKV-NKQSLSPLTAAKLAKKEMFDEILLEGDSV----- 358		
Qy	403	SRKPKDWAYGPVYSLSYDLSSLDTCGE-----EASVLEILVYNSKIENRHEMLAVEPIN 456		
Db	359	-----WAYGDASSTAYPLAKIDTINETTGELNEASALSVMYQGTVE--HLELDGLD 410		
Qy	457	ELLRDKWRKFG---AVSFYINVSYLCAWIFTL-----TAYYOPLEG- 496		
Db	411	TLLEAKWEAFAKRNWIVSFTAFLLYICFVTAFTLRPIGFSTEMTEGWINRYSEFPGR 470		
Qy	497	-----TPPYPTRTVDYLRAGE---VI 516		
Db	471	YGNKSTLQQVKVPVINATSRGLVENSEPLSQCHLRNWDPIPFANS--YIRLVFELFVVI 528		
Qy	517	TLFGVLFFFTNIKDLFWKKCPGVNSLF-IDGSFOLLYFIYSVLVIVSAALYLAGIEAYL 575		
Db	529	GICQVQFLDFRDIKRIGKKWMNVLTAPAKITFLKTYFLVLAMITPRACDLSVLLVW 588		
Qy	576	--AVWFEALVGMNNAlyFTRGKLKTGTYSIMIOKFLFKDLFRLLVLLFMIGVYASALV 633		
Db	589	DNVLITVTMTFTTHYLYYCRVIRFVGPFVLMVYTIATDIFRMLIYGIFLMGFSQSF 648		
Qy	634	SLNLC-----AN-MKVCNEDQNCIT-----VPTYSC--RDETFES----- 667		
Db	649	LIFLSCREANVIRKLLITDOSEAGSDGNKFNLRQISAYDTAIVKNAEVENVMQSPIE 708		
Qy	668	-----TFLLDLFKLIGMGDEMLSTKYVPVFIILLTYIILTFVLLNMLIALMG--E 720		
Db	709	AFVETFTLTGFTVLVRNALCALCPANTMWIGKVYFILFELFVSIMQFNMLIAMTRYE 768		
Qy	721	TVGQVSKESHKHWKLOWATTILDIERSF-----PVFLRKAFRSSEMVTYCK 766		
Db	769	TIFOTQLE---YKQRAQVILMLELSLSPKERHOYLLKSRPTGTNNKTRS---LVVSK 821		
Qy	767	SSDGTDPDR 775		
Db	822	KSASFSDSK 830		

## RESULT 9

T20312  
 Hypothetical protein F28H7.10 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C:date: 13-Oct-1999 #sequence\_revision 15-Oct-1999 #te  
 C:Accession: T20312  
 R:Matthews, P.  
 submitted to the EMBL Data Library, June 1996



A:Reference number: Z19255  
A:Accession: T20312  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-790 <WIL>  
A:Cross-references: EMBL:274030; PIDN:CAA98449.1; GSPDB:GN00023; CESP:F28H7.10  
A:Experimental source: clone D1054  
R:Birks, M.  
submitted to the EMBL Data Library, May 1996  
A:Reference number: Z19435  
A:Accession: T21533  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-790 <WIL2>  
A:Cross-references: EMBL:272508; PIDN:CAA96644.1; GSPDB:GN00023; CESP:F28H7.10  
A:Experimental source: clone F28H7  
C:Genetics:  
A:Gene: CESP:F28H7.10  
A:Map position: 5  
A:Introns: 46/2; 89/3; 129/1; 157/1; 201/1; 264/2; 349/3; 406/3; 487/3; 543/2; 580/1; 67

Query Match 7.5%; Score 342.5; DB 2; Length 790;  
Best Local Similarity 22.3%; Pred. No. 1.3e-16;  
Matches 167; Conservative 99; Mismatches 221; Indels 263; Gaps 30;

QY 152 PILEFIVSRGSTADLGLLPLFLTHKKRL-----TDEFR-----PSTGK 192  
DB 109 PNILDEPDQO-AEMAGDL-----KKALLDGGGKGKSKYREMYWWSVDERGSMGE 161  
QY 193 TCLPKALLNLNNGRNDTIPVLLDIAERTGN-MREFNISPRDIYRGQATALHAIERCK 251  
DB 162 NLIAICLQGSALHN-----LIARLINFPLKINDICVSEYGLSLPLHAIYNQDA 214  
QY 252 HYVELLVAOGADYHAQARGFPQKDE-----GGYFFGELPLS 290  
DB 215 QFTSLLRLGLADLNQRCYGAFFCADDQKASRTDSLEHEFVELKNTNYTGSYFGEYPLS 274  
QY 291 LAACINQPHVINYLTENPHKKADMRRQDSRGNTVHALVAIAADNTRENTKFTVMYDLLLL 350  
DB 275 FAICMGHDLFRMLLA---KKALSAQDNTNGNTALH-LCVIHD-----KM-DML- 318  
QY 351 LKCARLPDPSNLEA-----VLNNDGLSPLMAAKTGKIGIFQHIIRREVTDTRHLSRK 405  
DB 319 -----DAVLEAGNIRLANKQNTALTALAK-----KTESIQHLE-- 356  
QY 406 FKDAYGPVYSSYLLDSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRK 465  
DB 357 -----LMDGLIEQILDEKKA 372  
QY 466 FGAVSFYINVSVYLCAMVITLTAYQPLEGTPPYPTVTD----- 507  
DB 373 YGRALWRLSLGFIFFYCCFVCAIMLRPSSATTEHLTRGRINDDGETESTNSTNYLQWHA 432  
QY 508 -----YLRLAGEVITLFT---GVLFETNIKDL-----FMKKCPG 539  
DB 433 IDTOCHLMYSANPWTHGWFRGCEIMTIIVFQILLDFGIRRGFKWFLKAFPA 492  
QY 540 VNSLFDGSQLLYFIVSVLVISAALYAGIAYLAV-----MVFALVLGMMNALYFTRG 595  
DB 493 --KLMPKGAFLFIISIPCLACSFH---EFFLTIDNTMAIISILLVTHQFLYLMRA 544  
QY 596 LKITGYSIMQILFKDFRLLVLLFMIGVASALVSLNCPANKKVCNEDQNTCTVP 655  
DB 545 IPEVGPFLVMVYTIATDLVRFAMYSIFLVGSQSFLYFTSC----- 589  
QY 656 TYPSCRDSETF-----STF-----LLDLFKLTIGMDL---EMLSKTKPVVF 695  
DB 590 -----RDSIAIKIDPMGSEFNMINENPVALLRTFIMTIGESVLYREMSACDNFMWK 644  
QY 696 IILLVTVIILTFVLL--NMLIALMG---ETVQGVSKESHKHWKQWATTILDIERSF-- 748  
DB 645 IGLKLVIFETFSVLIQFNLLIAMMTTETIFLTRKE----WKQAWQVILMEGLSP 700

QY 749 -----PVFLRKAFRSGEMTVVGK 766  
DB 701 ASRKMHLLRYTRTGINKRVSRYVVSKEG 730

RESULT 10  
T24772  
hypothetical protein T10B10.7 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T24772  
R:Sims, M.  
submitted to the EMBL Data Library, May 1996  
A:Reference number: Z19934  
A:Accession: T24772  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-519 <WIL>  
A:Cross-references: EMBL:272514; PIDN:CAA96679.1; GSPDB:GN00028; CESP:T10B10.7  
A:Experimental source: clone T10B10  
C:Genetics:  
A:Gene: CESP:T10B10.7  
A:Map position: X  
A:Introns: 47/3; 139/1; 183/1; 215/2; 249/2; 385/3; 440/3

Query Match 6.1%; Score 278; DB 2; Length 519;  
Best Local Similarity 29.5%; Pred. No. 3.5e-12;  
Matches 89; Conservative 36; Mismatches 115; Indels 62; Gaps 10;

QY 216 IARTCNMREFINSPF-RDIYR--GOTALHIAIERCKHYVELLVAOGADYHAQARGRF 272  
DB 161 VKMTYRFKIVNDIFLSEYASVGLSPLHQAIYNEDLEMYFLCKGADVHORCYGSF 220  
QY 273 FQPKDE-----GGYFFGELPLSLAAGTNPQPHIVNYLTENPHKK 311  
DB 221 FCADDQKASRTDSLEHEWVDLVOSTKYTGMYGVEYPLSFAACTNQVDCFRLLRA---MK 277  
QY 312 ADMRRQDSRGNTVHALVAIAADNTRENTKFTVMYDLLLLKCARLPDPSNLEAVLNNDGL 371  
DB 278 ADPNMPTDNGNTVLH-----LTVIHDLPENFMLJAVELGANLH-VRNNKL 321  
QY 372 SPLMAAKTGKIGIFQHIIRREVTDTRHLSRKQWAGVYVSSYLLDSSLDTCGEE- 430  
DB 322 TPLAALAKLAKHIIYDILE---CDMDI-----SWRYGPVCKAYPLNDVDTINESD 370  
QY 431 -----ASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSVYLCAMVIF 485  
DB 371 GSNLPSNVIANVYVGKVD--HLEFFDGLIEEVLESKWETFGKKQLFMSLAGVIYFLAVF 428  
QY 486 TL 487  
DB 429 YL 430

RESULT 11  
T19552  
hypothetical protein C29E6.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T19552  
R:Dobson, R.  
submitted to the EMBL Data Library, May 1996  
A:Reference number: Z19141  
A:Accession: T19552  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1188 <WIL>  
A:Cross-references: EMBL:272504; PIDN:CAA96603.1; GSPDB:GN00022; CESP:C29E6.2  
A:Experimental source: clone C29E6  
C:Genetics:  
A:Gene: CESP:C29E6.2  
A:Map position: 4  
A:Introns: 147/2; 473/3; 500/1; 529/1; 584/2; 688/2; 839/3; 975/3; 1132/3

Query Match 5.1%; Score 235.5; DB 2; Length 1188;  
Best Local Similarity 20.1%; Pred. No. 1.4e-08;  
Matches 168; Conservative 113; Mismatches 280; Indels 273; Gaps 37;

QY 124 RKIIKQPOSPKAPQPPPIIKVFNRPILFDIVSGSTADLD-----GLLPFLLT 175  
DB 418 RKNKETERSALKSPTRNTLRIVSEVDRVTMVNVDRDQNTPMHIVASNGYLEMMOLLOK 477  
QY 176 HKRLT---DEEFEPSTGKCLPKALLN-----SNG 205  
DB 478 HGASITQVNEDEE-----TALHRAAGVROLLEWDIRLLMKDMGMSALHLAARS 529  
QY 206 RNDTIPVLLDIAERTGNMREFINSFRDIYRGQTALHIAIERCKHYVELLVAQADVH 265  
DB 530 HDATTKVLLD-----NGADREAKNS-----YQ-KTPOVAVDSGKLETGORLVAKGAIE 578  
QY 266 AQ-----ARGRFQPKDEGGYFYFGEPLSLAUCANQPHIVN 302  
DB 579 SSSDTKTVLHTAAYGNESIVRYFIAEGVTIDRRDEEGKTAFD-----IAC-----624  
QY 303 YLTENPHKKADMR---ODSRGNTVLHALVAIAD-----NTRENTKF---VTWKYDLL 349  
DB 625 ---ENDHK---DVARAELETQWKNLMPICDVIPLDKHRNPVNMKRRTPFTLLTKPELA 679  
QY 350 -----LLKCARLPDSNLEAVLNNDGLSPLMAAKTGKIGIFQHIIR-REVTDDETRHL 402  
DB 680 SFVMDNCIEKSEETDSTOSVAYNFEFLDDTYMMRCVSDGDTGEQLGCKSADED---735  
QY 403 SRKFKQWAGPVYSSLYDSSLDTCGEEASVLILVYN-----SKTENRHEMLAVPEINE 457  
DB 736 ---FKLEDAQSVASNYD-----RVYKYHPLKLMADAIEKLH--LLNHPLSK 776  
QY 458 -LLRDWRKRFAGSVFINVSYLCAMVIFTLTAYQPLEGTPPYRTVDYLRAGEVI 516  
DB 777 ALUKYKWNRLGRMPYIFALFMYL--VFIVSLTOYVRHTKA-----PYNWNEESYDSE-- 828  
QY 517 TLTGTGLVFFFTNKIDLFMKKCPGVNSLFD-----GSFQLLY-----553  
DB 829 -----YFDEN-----ETCPOINTTKPDVWVKIIQITLAVCQILVECFQPKRFAVL 875  
QY 554 -----FIKSVLVIV---SAALYLAGIEAYLAWVFALVL--GWNMALLYFTTGLKL 598  
DB 876 VMWENNIDCFIYSTATIYDFSECSATSGVRNQMOWILAALCFFGWINLLPMIRKMPR 935  
QY 599 TGYSTMIQIKFLKDLFRLLVLLPMIGVASALVSLNLPANCKANVCNEDOTNCTVPTYP 658  
DB 936 FGIVFVNFVDIV-KTFRFPFVFLVFIASFSSFYVIL-----972  
QY 659 SCRDSFTFTLLDLFLKLTGM-----GD-----LEMLSTKYPVVFILLVTYI 703  
DB 973 --QNRPEFSTIFMSPLKTVMMIGEFETGIFGHDETTHAEKMFQPAHTAVACALFFFC 1030  
QY 704 ILTFVLLNMLIALMGETVGVQSKSHIWKQLQWATTILDIERSPFVFLRK-----754  
DB 1031 IIMTILLNLLGLAVDDIKGVOEKAEKRLAMQVLDVLQIEASLHFFIORTKRYATCRY 1090  
QY 755 -AFRSGEMTVGKSSDGTDRRCFRVDEVNWSHWNQNLGI-INEDPGKNETVQ 806  
DB 1091 ATPPYKLUKTKTGAG-----W-----WSNFRRRFGLSVSTDPDEIDEME 1129

RESULT 12  
JC5807  
trp3 protein - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 07-May-1999  
C:Accession: JC5807  
R:Preutz, K.D.; Noeller, J.K.; Krause, E.; Goebel, A.; Schulz, I.  
Biochem. Biophys. Res. Commun. 240, 167-172, 1997  
A:Title: Expression and characterization of a trp1 homolog from rat.  
A:Reference number: JC5807; MUID:98042538; PMID:9367904  
A:Accession: JC5807

A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-828 <PRE>  
A:Experimental source: brain  
C:Comment: This protein participates in store-operated Ca2+ entry into cells.  
C:Superfamily: TRPC3 protein

Query Match 4.1%; Score 188; DB 2; Length 828;  
Best Local Similarity 20.6%; Pred. No. 2.4e-05;  
Matches 137; Conservative 100; Mismatches 240; Indels 188; Gaps 31;

QY 210 IPVLLDIAERTGNMREFINSFRDIYRGQTALHIAIERCKHYVELL-----VAQADV 264  
DB 52 IPVVRKMLEBSRTLN--VNC-----VDYMGONALQAVGNEHLEVTTELLKKENLARIGDA 105  
QY 265 -----HAQARGFFQF---KDEGGYFYFGE-----LPLSLAA 293  
DB 106 LLLAISKGVYRIVEAILSHPALAQOQTLSPLEURDDD--FYDEDDTRFSPTDTPILAA 163  
QY 294 CTNQPHIVNVL-----TENPH-----KKADMRRD-----SRGNTVLHALVAIADNT 335  
DB 164 HCHKYEVVHLLLLKGRTERPHDYLCRCADCAEKQRLMTFSHSRINAYKASPGVLSLS 223  
QY 336 RENTKFTVMYDLLLLKCARLPDSNLEAVLNNDGLSPLMAAKTGKIGIF-----386  
DB 224 SEDPVLTALELSNELAKLA-----NIEKEFKND--YRKLSMOCKDFVGVLDLCRDSEEV 276  
QY 387 OHIRREVTDDETRH-----LSR-----KFKDWAYGPVYSSLYDSSLDTCGEEASV- 433  
DB 277 EALNGDLSVEERHGHKASLSRVKLAIKYEVKFKVAPNCOOQLLTWYGNLSGRETAK 336  
QY 434 -LEILVYNSKIENRHEMLAV-----EPINELLRDWRKRFAGSVFINVSYLCAMVIF 485  
DB 337 CLVVLVVALAL---PFLAIGYWIAPCSRGLKILRSFPMKFAASFI---FLGLLVF 387  
QY 486 TLTAYQPLEGTPPYRTVDYLRAGEV-ITLFTGV-LFFFTNKIDLFMKKCPGVNSL 543  
DB 388 NASDRF---EGITTLNITVIDYKQIFRVTQFTWTEMLIMVVLGMMWSEC---KEL 441  
QY 544 FIDGSPQLLYFYISVLIVS-----AALYLAGIEAYLA-----576  
DB 442 WLEGPREYIVQLMNVNLDLFIATAFTARFLAQTKAQOYVDSHVQESDLEVTLPPEV 501  
QY 577 -----VMVFALVGLGMMNALYFTRGLKLTGYSTMIQIKFLKDLF 615  
DB 502 QYFTYARDKWLPSDPOIIEGLYAIIVLSFSRIAIVLPANESFGPLQISLGRTV-KDIF 560  
QY 616 RELLVYLLPMIGVASALVSLNLPANCKANVCNEDOTNCTVPTYPSCRDSEFTFLDLDFK 675  
DB 561 KFWLFIWVFLAFMIGMFIYSYLGAKV---DPAFTTV-----EESFKTLFWSIFG 609  
QY 676 LTIGMDLEMLST-KYPVVF-----ILLVTYILTFVLLNMLIALMGETVGVQSKES 729  
DB 610 LS-----EVTSVLAYDKHFTENIGYVLYGIYNTVMVVLNMLIAMINSSYQIEEDS 663  
QY 730 KHIWK 734  
DB 664 DYEMK 668

RESULT 13  
JH0588  
calmodulin-binding protein trpl - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 01-Mar-2002  
C:Accession: JH0588  
R:Phillips, A.M.; Bull, A.; Kelly, L.E.  
Neuron 8, 631-642, 1992  
A:Title: Identification of a Drosophila gene encoding a calmodulin-binding protein  
A:Reference number: JH0588; MUID:92232293; PMID:1314616  
A:Accession: JH0588  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA

A:Residues: 1-1124 <PH>  
A:Cross-references: GB:M88185; NID:9469057; PID:gl58715  
A:Experimental source: head  
C:Genetics:  
A:Gene: trpl  
C:Superfamily: TRPC3 protein  
C:Keywords: calmodulin binding; phosphoprotein; transmembrane protein  
F:341-362/Domain: transmembrane #status predicted <TM1>  
F:374-396/Domain: transmembrane #status predicted <TM2>  
F:462-479/Domain: transmembrane #status predicted <TM3>  
F:512-533/Domain: transmembrane #status predicted <TM4>  
F:549-572/Domain: transmembrane #status predicted <TM5>  
F:643-668/Domain: transmembrane #status predicted <TM6>  
F:710-727/Region: calmodulin binding #status predicted  
F:722/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 3.2%; Score 148; DB 2; Length 1124;  
Best Local Similarity 19.0%; Pred. No. 0.03;  
Matches 148; Conservative 103; Mismatches 255; Indels 274; Gaps 36;  
QY 189 STGKTCLPALLNLSGRNDTPVLLD-----IAERTG---NMREFINSPFRDIYR--- 237  
DB 24 SVGGCCVPLGLPQ-----PILLEKKEFLAVERGDMPNRRILQKALRHQHINIC 74  
QY 238 ----GQTALHTAIERCKHYVELLVAQAD-----VHAQ 267  
DB 75 MDPLGRALTAIDNENLEMYVELLVGMVETKDALHAINAEFVEAVELLEHEELIYKE 134  
QY 268 ARGFRFOPKDEGGYFYGEL-PLSLAACNQPHVNVLTEN-----PH----- 309  
DB 135 GEPYSWQKVDINTAMFADITPLMLAAHKNFEILRILLDRGAAPVPHDRCGCECVR 194  
QY 310 --KKAMRRQDSRGN-----TVLHALVAIADTNTRETKF-----VTKM-----YDL 348  
DB 195 LTAEDSLRHSLSRNIYRALCSPSLICLTSNDSPSTAFQLSWELRNALATQOECKSEYMD 254  
QY 349 LLLKCARLFPD-----SNLEAVLNNDGSLPLMMAAKTGKIGFOHIIIRREVTDETR 400  
DB 255 LRROCKFAVDLLDQTRSRELATILNYD---POMSSVEPG-----DRM 295  
QY 401 HLSRKKFDWAYGP---VYSSLYDL-----SSLD--TCGEASV---LEI 436  
DB 296 SLTRLVQNAISYKQKFAHNSIQQLLSIWYDGLPGFRKRSIVDKVICIAQVAVFLPLYC 355  
QY 437 LVYNSKIENRHEMLAVEP INELLDRKWRKFGAVSYFINVSYLCAMVIFTLTAYIQPLEG 496  
DB 356 LIYWCAPNCRGTQGLMRKPF-----MKFLIHASSYLFELFILIVS----- 395  
QY 497 TTPYPYRTVDYDLRAG-----EVTILFTGVLFPTFNKDLF 533  
DB 396 ----QRADDDFVRIFGTRMKKELABEQELRQGTQPSKLELIYVMYVIGFWVEVEQEIF 450  
QY 534 MKKCPGVNSL-----FDGSGQLLYFYISVLVVSAAALYLAGIE-----AYLAVNVE 580  
DB 451 ----AVGKSYLRNWNWIDFLRNSLY--VSVWCLRAFAYTQATEIARDPQMAIYPREKW 505  
QY 581 -----ALVLGWMNALYFTRGLKLTGYSI-----MIQKLFK---DLFRFLLYLLFMI 626  
DB 506 HFDPPQLIAEGLFAAANVFSALKVLHLSINPHLGLQLISLRMVVIDIVKFFIYTLVLF 565  
QY 627 GYASALVSLNPNCAKMKVCHNDQNTCTVPTYP-----SCRSETFSTFLDLFK 675  
DB 566 AFACGLNOLLWYFAAL-----EKSQCYV--LPQGEADWGHGSDCKWRRFG-----NLFE 614  
QY 676 LT-----ICMGOLEMSSLSTKYPWF--IILLVYIITLTVLLNMLIALMGETVGQ 724  
DB 615 SSQSLFWASFGWGLDDFELSGIKSYTRFWGLLNFSGYSYINVLVLLNLLIAMNSYAM 674  
QY 725 VKESKHIWKIQ-----WATTILDIERFPVFLRKAFRSGEMVTYVKGSSDGTDPDRRCFRV 780  
DB 675 IDEHSDTEWKFAFTKLWMSYFEDSATLPPPF-----NVLPSYKWKVIRI 717

## RESULT 14

I38361  
TRPC1 protein - human  
C:Species: Homo sapiens (man)  
C:Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 04-Sep-1998  
C:Accession: I38361  
R:Wes, P.D.; Chevesich, J.; Jeromin, A.; Rosenberg, C.; Stetten, G.; Montell, C.  
Proc. Natl. Acad. Sci. U.S.A. 92, 9652-9656, 1995  
A:Title: TRPC1, a human homolog of a Drosophila store-operated channel.  
A:Reference number: I38361; MUID:96003837; PMID:7568191  
A:Accession: I38361  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-810 <RES>  
A:Cross-references: EMBL:X89066; NID:g1019786; PID:g1019787  
C:Superfamily: TRPC3 protein  
Query Match 3.0%; Score 138.5; DB 2; Length 810;  
Best Local Similarity 18.1%; Pred. No. 0.091;  
Matches 147; Conservative 126; Mismatches 315; Indels 223; Gaps 36;  
QY 12 PGEVAELPGDSESGTPGGEAPFLSSLANLFECEGDSLSPSPADASRPAGPGDGRPNLRMKF 71  
DB 3 PG-----IPGPRAEAAVGTTHPFSFGAWLGGSGS---GPVGAPPPS----- 42  
QY 72 QGAFRKGVNPIDILLESTLYESSYVPGPKAPMDSLFDYGYTRHHSSDNKWRKKIIEKQ 131  
DB 43 -----PGLPPSWAAMMAALYPSTDLSGASSSL----- 70  
QY 132 POSKAPAPQPPPIKLVNRPILPDIVSRGSTADLGLLPLFLTHKK---RLTDEEPRP 188  
DB 71 PSSPSSSSNEPVMAK-----DVREKVEENTLNEKL-FLLACDKGDYMYMKKILEEN 121  
QY 189 STGK---TCLP-----KALLNLSGRNDTPVLLD-----IAERTGMREFINSPFRDIY 235  
DB 122 SSGDLNINCVDVLRGNVTTIENENLDIQLLDYCCQKLMERIQNE---YSTWMDV- 177  
QY 236 YRGOTALHIAIERCKHYVELLVAQADV---HA-QARGRFOPKDEGGYFYGELPLSL 291  
DB 178 ----APVILAAHRNNEYILTMLLKQDVSLPKPAGVCECTLCSAKNKKDSLRSRFRLDI 233  
QY 292 AACTNQPHVNYLTENPHKKADMRQDSRGNTVHLHALVAIAD-----NTRENT 339  
DB 234 YRCLASPALIMLTEDP-----ILRAFELSADLKELSLVEVEFRNDYEEL 278  
QY 340 KFTVMYDILLKLCARLFPDSNLEAVLND-----GLSPLMMAAKTGKI 383  
DB 279 AROCKMFAKOLLAQAR--NSRELEVLNHTSSDEPLDKRGLLEBMMNLSRLKAIKYN-- 334  
QY 384 GIFQHIIRREVTDETRHLSRKFDWAYGPVYSLSYDLSLSDTCGEASVLEILVYNSKI 443  
DB 335 -----QKEFVSQSN---CQQLNTVW---FGMSGYRRKPTCKKIMTVLTGIF--- 377  
QY 444 ENRHEMLAVEPINELLRDKWRKFGAV-----SFYINVSVYLCAMVIFTL-TAYIQPLEG 496  
DB 378 -----WPVLSCLYIAPK-SQGRILHTFMKFIHGASYFTFLLLNLSLYSVDNKK 430  
QY 497 TTPYPYRTVDYDLRAGIEVITLFTGVLFNFTNKDLPMKKCPGVNSLFDIGSFOLLYFY 556  
DB 431 NTWGPALERIDYL-----LILWIIGMI--NSDIKRLAYE---GLED-FLEESRNLQSFVM 479  
QY 557 SVLVIVSAALYLAG-----TEAYLVNV-----FALVLGWMNALYFTRGLK 598  
DB 480 NSLYLATFALKVAHNKHFHDFADRKDWDADFHTLVAEGLFAFANVLSYLFRLFMYTTSSI 539  
QY 599 TGYISIMQIKLFDLFRLLVLLFMIGYASALVSLNPNCAKMKVCHNDQNTCTVPTYP 658  
DB 540 LGPLQISMGQML-ODFGKFLGMFLVLSFTIGLTQLYDKGYTSK-----EQKDC-VGIFC 593  
QY 659 SCRDSFTSFLLDLFLKLTIGMDLEMLSTKYPVVFII-----ILLVTVI 703  
DB 594 EQOSNDFTHSFICTCFAL-----FWIFSLAHVAIFVTRFSYGEELQSFVGAIVGTYN 647



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 3, 2003, 19:51:13 ; Search time 14 Seconds  
(without alignments)  
2577.458 Million cell updates/sec

Title: US-09-870-090A-2

Perfect score: 4577

Sequence: 1 MADSSGPRAGGEVAELPG.....PRCDGHOQGYPRKWRDTPAD 870

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	182	4.0	1172	1 TRP2_MOUSE	Q9r244 mus musculus
2	181.5	4.0	862	1 TRP7_HUMAN	Q9hcx4 homo sapien
3	178.5	3.9	862	1 TRP7_MOUSE	Q9hcx5 mus musculus
4	172	3.8	885	1 TRP2_RAT	Q9r283 rattus norv
5	166	3.6	981	1 TRP4_BOVIN	P79100 bos taurus
6	164	3.6	974	1 TRP4_MOUSE	Q9quq5 mus musculus
7	164	3.6	977	1 TRP4_HUMAN	Q9ubn4 homo sapien
8	161	3.5	977	1 TRP4_RAT	Q35119 rattus norv
9	155	3.4	1503	1 TRL2_HUMAN	Q94759 homo sapien
10	153	3.3	836	1 TRP3_MOUSE	Q9qzcl mus musculus
11	152.5	3.3	974	1 TRP5_RABIT	O62852 oryctolagus
12	150.5	3.3	973	1 TRP5_HUMAN	Q9ulb2 homo sapien
13	150.5	3.3	975	1 TRP5_MOUSE	Q9qx29 mus musculus
14	149.5	3.3	930	1 TRP6_MOUSE	Q61143 mus musculus
15	148	3.2	848	1 TRP3_HUMAN	O13507 homo sapien
16	148	3.2	1124	1 TRPL_DROME	P48994 drosophila
17	145	3.2	736	1 TRP2_RAT	Q9jmi9 rattus norv
18	143	3.1	931	1 TRP6_HUMAN	Q9y210 homo sapien
19	137	3.0	436	1 V245_FOWPY	Q9j425 fowipox vir
20	136.5	3.0	966	1 PKD2_MOUSE	O35245 mus musculus
21	135	2.9	1275	1 TRP_DROME	P19334 drosophila
22	134.5	2.9	968	1 PKD2_HUMAN	O13563 homo sapien
23	131.5	2.9	642	1 YAZA_SCHPO	Q09701 schizosacch
24	131.5	2.9	759	1 TRP1_RAT	Q9qx01 rattus norv
25	130.5	2.9	3056	1 ATM_HUMAN	O13315 homo sapien
26	129	2.8	823	1 YN52_CAEEL	P34586 caenorhabdi
27	128.5	2.8	759	1 TRP1_RABIT	Q9tun9 oryctolagus
28	127.5	2.8	4377	1 ANK3_HUMAN	O12955 homo sapien
29	126.5	2.8	768	1 YB23_HUMAN	Q9ulj7 homo sapien
30	126.5	2.8	2471	1 NTC2_RAT	Q9qwk30 rattus norv
31	125.5	2.7	809	1 TRP1_MOUSE	O61056 mus musculus
32	124	2.7	793	1 TRP1_HUMAN	P48995 homo sapien
33	123.5	2.7	793	1 TRP1_BOVIN	O18784 bos taurus

#### ALIGNMENTS

##### RESULT 1

ID	TRP2_MOUSE	STANDARD:	PRT;	1172 AA.
AC	Q9R244; Q9R243; Q9ES60; Q9ES59;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DE	Short transient receptor potential channel 2 (TrpC2) (mTrp2).			
GN	TRPC2 OR TRRP2 OR TRP2.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RC	TISSUE=Testis;			
RX	MEDLINE=99162557; PubMed=10051594;			
RA	Vannier B., Peyton M., Boulay G., Brown D., Qin N., Jiang M., Zhu X.,			
RA	Birnbaumer I.;			
RT	"Mouse trp2, the homologue of the human trpc2 pseudogene, encodes			
RT	mTrp2, a store depletion-activated capacitative Ca2+ entry channel.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 96:2060-2064(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).			
RX	PubMed=10998353;			
RA	Hofmann T., Schaefer M., Schultz G., Gudermann T.;			
RT	"Cloning, expression and subcellular localization of two novel splice			
RT	variants of mouse transient receptor potential channel 2.";			
RL	Biochem. J. 351:115-122(2000).			
CC	-1- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE			
CC	CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A			
CC	PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR			
CC	TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. MAY ALSO BE			
CC	ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).			
CC	-1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1/A (SHOWN HERE), 2/B, 3/ALPHA			
CC	AND 4/BETA; ARE PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- TISSUE SPECIFICITY: ISOFORM 3 IS UBQUITOUSLY EXPRESSED AT LOW			
CC	LEVELS. ISOFORM 4 IS EXPRESSED EXCLUSIVELY IN VOMERONASAL ORGAN.			
CC	-1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STREP			
CC	SUBFAMILY.			
CC	-1- SIMILARITY: CONTAINS 3 ANK REPEATS.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	EMBL; AF111108; AAD17196.1; -			
DR	EMBL; AF111107; AAD17195.1; -			
DR	EMBL; AF230803; AAG29951.1; -			
DR	EMBL; AF230802; AAG29950.1; -			
DR	MGI; 109527; Trp2.			

PI9838 homo sapien  
P54282 rattus norv  
Q04721 homo sapien  
Q35516 mus musculus  
Q9hcf6 homo sapien  
Q95271 homo sapien  
P97445 mus musculus  
Q9y566 homo sapien  
P57078 homo sapien  
Q07008 rattus norv  
Q02357 mus musculus  
P16157 homo sapien

DR InterPro: IPR002110; ANK.  
DR InterPro: IPR002111; Cat\_channel\_TrpL.  
DR InterPro: IPR000636; M+channel\_nlg.  
DR InterPro: IPR002153; Trans\_recep.  
DR InterPro: IPR002706; Xrccl\_N.  
DR Pfam: PF00520; ion\_trans; 1.  
DR Pfam: PF01834; XRCCL\_N; 1.  
DR PRINTS: PR01097; TRNSRECEPTR.  
DR PRODOM: PD023136; Xrccl\_N; 1.  
DR SMART: SM00248; ANK; 1.  
DR PROSITE: PS00088; ANK\_REPEAT; FALSE\_NEG.  
DR PROSITE: PS0297; ANK\_REPEAT\_REGION; FALSE\_NEG.  
KW Ionic channel; Transmembrane; Ion transport; Calcium channel;  
KW ANK repeat; Repeat; Alternative splicing.  
FT DOMAIN 1 659 CYTOPLASMIC (POTENTIAL).  
FT TRANSSEM 660 702 POTENTIAL.  
FT DOMAIN 681 702 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 703 723 POTENTIAL.  
FT DOMAIN 724 738 POTENTIAL.  
FT TRANSSEM 739 759 POTENTIAL.  
FT DOMAIN 760 789 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 790 810 POTENTIAL.  
FT DOMAIN 811 833 POTENTIAL.  
FT TRANSSEM 834 854 POTENTIAL.  
FT DOMAIN 855 899 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 900 920 POTENTIAL.  
FT DOMAIN 921 1172 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 301 330 ANK 1.  
FT REPEAT 377 406 ANK 2.  
FT REPEAT 430 459 ANK 3.  
FT DOMAIN 1140 1143 POLY-SER.  
FT VARSPLIC 1 111 MLMSRTDSKSGKNSRVNFMKDGDFLTPASGESWDRRLTSC  
FT SPTFTRHQSFLGLAFRLVRSLGLADFPVDPSPGSSGLNQ  
FT NSTDVLESOPRPLWLTNPSTRTTFFPDPT -> MGTKTHV  
FT VPW (IN ISOFORM 2).  
FT MISSING (IN ISOFORM 4).  
FT MISSING (IN ISOFORM 3).  
FT LVPK -> DPLS (IN ISOFORM 4).  
FT R -> K (IN REF. 2).  
FT S -> F (IN REF. 2).  
FT CONFLICT 633 653 Q -> R (IN REF. 2).  
FT CONFLICT 653 653 Q -> Y (IN REF. 2).  
FT CONFLICT 774 774 T -> A (IN REF. 2).  
FT CONFLICT 797 797 L -> P (IN REF. 2).  
FT CONFLICT 1161 1161 L -> P (IN REF. 2).  
SQ SEQUENCE -1172 AA; 130467 MW; B6A6F4BB941E946 CRC64;

Query Match  
Best Local Similarity 19.1%; Pred. No. 0.00043;  
Matches 189; Conservative 120; Mismatches 350; Indels 332; Gaps 40;

QY 8 PRAGGEVAELPGD-----ESGTPGGEAFPLSSLA-----NLFEGEDGSLSPSPA 52  
Db 109 PQTSTKEISELKMLKQLOPGLGRARMVLSAARKAPASVVSNNSHGEPG---PSRA 165  
QY 53 DASRPAGDGRNLRMKQGAFRKGVNPDIDLESTLYESSVVGPKKAPMDSLFYDGT 112  
Db 166 ESAPRAE---EPNRTAVGRARRKRVQEP-----RRSLNSSSQPNRRGT-----R 211  
QY 113 YRHSSDNKRWRKI-----IEKQSPKAPAPQPPPIKLVFNRPILFDIV 158  
Db 212 QROHRPOTKSDGCVQAQCPCACAGFFSTETLPQHAATCGESPPP-----257  
QY 159 SRGSTADLGLFLTLTHKKRLT-----DEEFREPST-----OKTCL 195  
Db 258 QPASASLSSSESVLRHRRHVALTPVLPKQPNMTEIVNKKLKFPTLLRAIQEGQLG 317  
QY 196 PRALLNLSGRNDTIP-----VLLDIAERTGN-----WREINSPFRD 233  
Db 318 VOOLLESSDASGAGPGPLRNVESEDRSWREALNLAIRLGHVITDVLNANVKDFDQ 377  
QY 234 IYRGOTALHIAIERCKKHVELLVA-----OCADVHAQARG--RFQPKDEGGYFYFGE 287  
Db 378 IH-----EALLVAVDTHQPAVRRLLARLEREKGRKVDTKSFLAFFDSSIDGSRFAPGV 433

QY 288 PLSIACTNPHIVNYLTENPHKKADMRRODSRGNTVYLHALVAIADNTRENTKFTKMYD 347  
Db 434 PLTLACQKDLYEIAQLLMDQHTIA-----RHPVSCACLECSNARR-----YD 477  
QY 348 LLLKLCARLPFDSNLEAVLNDGLSPMLMAAKTGKIGIFQHIIRREYVTDDETRHLSRKF 407  
Db 478 LKFLSLRSI---NTYRGIASRAHLS---LASEDAMLAFAO--LSREL-----RRLARKEP 524  
QY 408 DWAYGPVYSSL-----YDLSLSDTC---GEEASVLEILVYNSKIENRHEMLA---VEPI 455  
Db 525 E--FKQYIALESQCQDYGFELOWCRNQSEVTAVLDGDESETETEPAGLQCAFEGE 582  
QY 456 NEILLRDK-----VSFYINVSVYLCAMVI-----FILTAYYQPLEGTPPYR 503  
Db 583 PNLARLRVAVNKKQFVAHPICQOVLSIWCNGLAGWGSTTIWRLFVASFILTMPFL 642  
QY 469 -----VSFYINVSVYLCAMVI-----FILTAYYQPLEGTPPYR 503  
Db 643 CIGYWLAPKSQLGRLLKIPVKFLLHSASYLWFLFLLGESLYMETQSLTFKGRSOSVWE 702  
QY 504 TTVLYRLAGEVITLFTGVLFFTNFKDLPKPCGVNSLFDIGSFQLLFYIYSVLVIVS 563  
Db 703 TSLHMIWVG-----FLMECKEYWE---GLRSYLLDW-----WFLDQVVI 741  
QY 564 AALYLAGI-----EAYLAVVWFAL--V 583  
Db 742 LSLYLASFALRLLLAGLAVMHCDA SDSTTCRCFTTAERSEWRTDPOFLAEVLFTVSM 801  
QY 584 LGHMNALYFTRGLKLTGYSIMIOKILFKDLRFLLVYLLFMIGYASALVSLNPCANMK 643  
Db 802 LSFTRLAYILPAHESLGTLQISIGKMI--DDMIRFMFLMIILTAFLCGL-----849  
QY 644 VCNEDTNTCTVPTPSCROSETPSTFLDLFLKLTIGMDLEMLSSTKYPVVFILLVTVI 703  
Db 850 -----NNIYVP--YQSEKLGNFNETFQFLFTWFMCGEHTVVYDMQFLVPEVGRAMYG 902  
QY 704 ILTFVL---LLNMLIALMETVQVSKSHIWKLOWATTILDIR---SFPV-----750  
Db 903 IFTVMVIVLLNMLIAMITNSFKIEDDADVENKFAKSKLYLSYFREGTLTPVPFFNILPS 962  
QY 751 -----FLRKAPR---SGEMVTYVGSKSDGTP 772  
Db 963 PKAIFYLVRIRFRFLCCGSCCKAKKASDIPP 993

RESULT 2  
TRP7\_HUMAN STANDARD; PRT; 862 AA.  
ID TRP7\_HUMAN  
AC Q9HCX4;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Short transient receptor potential channel 7 (TrpC7) (Trp7 protein).  
GN TRPC7 OR TRP7.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Murphy C.T., Li S., Jordan N.J., Reaves B.J., Wolstenholme A.J.,  
RT Westwick J.;  
RT "Distribution of a novel human capacitative calcium entry channel;  
RT htrp7";  
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE  
CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A  
CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR  
CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. ACTIVATED BY  
CC DIACYLGLYCEROL (DAG) (BY SIMILARITY). MAY ALSO BE ACTIVATED BY  
CC INTRACELLULAR CALCIUM STORE DEPLETION.



```

CC EMBL; AF139923; AAD42069.1; -
DR MGD; MGI:1349470; Trp8.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR000636; M_channel_nlg.
DR InterPro; IPR002153; Trans_recep.
DR InterPro; IPR004729; Trp_CaChannel.
DR Pfam; PF00023; ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01097; TRNSRECEPTR.
DR SMART; SM00248; ANK; 1.
DR TIGRfams; TIGR00870; trp; 1.
DR PROSITE; PS00088; ANK_REPEAT; FALSE_NEG.
DR PROSITE; PS0297; ANK_REPEAT_REGION; FALSE_NEG.
KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW ANK repeat; Repeat; Glycoprotein.
FT DOMAIN 1 351 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 352 372 POTENTIAL.
FT DOMAIN 373 383 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 384 404 POTENTIAL.
FT DOMAIN 405 465 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 466 486 POTENTIAL.
FT DOMAIN 487 537 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 538 558 POTENTIAL.
FT DOMAIN 559 581 CYTOPLASMIC (POTENTIAL).
FT TRANSEM 582 602 POTENTIAL.
FT DOMAIN 603 651 EXTRACELLULAR (POTENTIAL).
FT TRANSEM 652 672 POTENTIAL.
FT DOMAIN 673 862 CYTOPLASMIC (POTENTIAL).
FT REPEAT 42 71 ANK 1.
FT REPEAT 77 106 ANK 2.
FT REPEAT 108 134 ANK 3.
FT REPEAT 163 192 ANK 4.
FT REPEAT 563 592 ANK 5.
FT CARBOHYD 514 514 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 862 AA; 99474 MW; C2E2CE1A6A9FC3D CRC64;

Query Match
Best Local Similarity 3.98; Score 178.5; DB 1; Length 862;
Matches 146; Conservative 105; Mismatches 258; Indels 221; Gaps 33;

QY 185 FRPSTGKTCLPALLNLNGRNDTPVLDIAERTGNMREFNSPRDIYRGQTALHI 244
DB 33 FNEKGTSLT--PEERFLDAEYGNIPVVRKMLESKTLN-----FNCVDYMGQNALQL 84
QY 245 AIERRCKHYVELLV-----AOG-----ADVHA 266
DB 85 AVGNEHLEVTLELLKKENLARVGDALLAISKGVRIVEAILSHPAFAQORLTSLPLEQ 144
QY 267 QARGRFQPKDEGGYFYFGEI-PLSLAACTNQHIVNVL-----TENPH-----KKA 312
DB 145 ELRDDDIFYAYDEGDTFRSHDITPILAAHCQVEIVHILLKGARIEPHDYCKCNECT 204
QY 313 DMRRQD---SRGNTVHLVAIAONTRENTKFTKMYDLLLL--KCARLFPDSNLEAVLNN 368
DB 205 EKORKDSFHSRSMNAYKGLAAYLSLSEDPVLTALSNEARL---ANIETEFKN 261
QY 369 DGLSPLMMAKTGKIGIF-----QHIIREV-----TDSDTHLSR-----KFK 407
DB 262 D-YRKSUQCKDFVGVLDLCRDETEVEAILNGDVLNQVSDHHRPSLSRIKAIKVEVK 320
QY 408 DWAYGP-----VYSSLDLSLSDTCCEASVLEILVYNSKIENRHEMLAVEPINEL 458
DB 321 KFAVHPNCOOQLTMWYENLSGLRQOSIAVKFLAVFGVSLGFLFATAYWIAPCSKLGQT 380
QY 459 LRDKWRKF--GAVSFYINNVSYLCAMVIFTLTAYOPELGTPPYRTTVDYLRAGEVI 516
DB 381 LRSPFMKFAVAHVSFTI---FLGLLVNNSDRF---EGVKTLPLNETFDYKQIPRVK 432
QY 517 TLTGTGLVFFFTNIKIDFMK-----KCP-----GVNSLFDGS 548
DB 433 T-----TQFSWTEM--LIMKWVLGMWSECKEIVEGPREYVHLWNLNLLDFGMLSIYV-AS 485

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QY 549 F-----QLLYFTY-----SVLVIVSAALYL 568
DB 486 FTAREMAFLKASEAQLVVDQVQVDTLHNVSLPEVAYFTYARDKWPSPDQIIISGLY- 544
QY 569 AGIAYLAVWVFLVGLWMNALYFTRGLKLTGYTSIMQIKLFDLFRFLVLLYLLFMIGY 628
DB 545 -----AIAVVLFSRIAYILPANESFGPLQISLGRTV-KDIFKFMVIFIMVFAV 593
QY 629 ASALVSLNPNCAKMKVCNEDQTNCTVPTPSCRDSETFSTFLDLFLKLTIGMGDLEMLSS 688
DB 594 ---NIGMFLYSYRGAKYNPAFTV-----EESFKTLFWSIFGLS-----EIVSV 636
QY 689 T-KYPVFI-----ILVTYIILTFVLLNNLIALMGETGVQVSKESKHVQLQWA---T 739
DB 637 VLKYDHKFIENIGVLYGVYNTVMVYVLLNNLMIAMINNSYQETEEADADVEWKFARAKLWL 696
QY 740 TILDIERSP 749
DB 697 SYFDEGRTLP 706

RESULT 4
TRP2_RAT
ID TRP2_RAT STANDARD; PRT; 885 AA.
AC Q9R283;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Short transient receptor potential channel 2 (TrpC2) (rTRP2).
GN TRP2 OR TRP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99254120; PubMed=10318963;
RA Liman E.R., Corey D.P., Dulac C.;
RT "TRP2: a candidate transduction channel for mammalian pheromone
RT sensory signaling.";
RL Proc Natl Acad Sci U S A. 96:5791-5796(1999).
CC -1- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED CALCIUM PERMEANT
CC CATION CHANNEL. PROBABLY IS OPERATED BY A PHOSPHATIDYLINOSITOL
CC SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR TYROSINE KINASES OR
CC G-PROTEIN COUPLED RECEPTORS. IS NOT ACTIVATED BY INTRACELLULAR
CC CALCIUM STORE DEPLETION.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN VOMERONASAL ORGAN
CC NEURONS (SENSORY MICROVILLI).
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 3 ANK REPEATS.
CC -----
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CC -----
CC EMBL; AF136401; AAD31453.1; -
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR000636; M_channel_nlg.
DR InterPro; IPR002153; Trans_recep.
DR Pfam; PF00023; ank; 3.
DR Pfam; PF00520; Ion_trans; 1.
DR PRINTS; PR01097; TRNSRECEPTR.
DR SMART; SM00248; ANK; 1.
DR PROSITE; PS00088; ANK_REPEAT; FALSE_NEG.
DR PROSITE; PS0297; ANK_REPEAT_REGION; FALSE_NEG.

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Ionic channel; Transmembrane; Ion transport; Calcium channel;  
ANK repeat; Repeat.

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QY 716 ALMGETVGQVSKESKHVWKLQWATTTILDIER---SPVV-----FLRKAPR-- 757
||: : : : : || | : : ||
Db 634 AMTNSPQKIDEDADVEMKFARSKLYLSPFREGILTLPVPFNILPSPKAAFYLLRRIFRFI 693
||: : : : : || | : : ||
QY 758 -SGEMVTGKGSSDGP 772
|| | | | |
Db 694 CCGSSCCCKARKSDYPP 709
|| | | | |

RESULT 5
TRP4_BOVIN
ID TRP4_BOVIN STANDARD; PRT; 981 AA.
AC P79100;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Short transient receptor potential channel 4 (TrpC4) (Capacitative
DE calcium entry channel 1) (CEEL).
DE TRPC4.
GN Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A. (ISOFORM ALPHA).
RP TISSUE=Retina, and Adrenal gland;
RC MEDLINE=97102798; PubMed=8947038;
RX Philipp S., Cavalle A., Freichel M., Wissenbach U., Zimmer S.,
RA Trost C., Marquart A., Murakami M., Flockerzi V.;
RA "A mammalian capacitative calcium entry channel homologous to
RT Drosophila TRP and TRPL.";
RT EMBO J. 15:6166-6171(1996).
RN [2]
SEQUENCE FROM N.A. (ISOFORM BETA).
RP TISSUE=Adrenal gland;
RC MEDLINE=98158580; PubMed=9498815;
RX Freichel M., Wissenbach U., Philipp S., Flockerzi V.;
RA "Alternative splicing and tissue specific expression of the 5'
RT truncated bCCE 1 variant bCCE Idelta514.";
RT FEBS Lett. 422:354-358(1998).
CC -1- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE
CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A
CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR
CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN
CC SHOWN TO BE CALCIUM-SELECTIVE. MAY ALSO BE ACTIVATED BY
CC INTRACELLULAR CALCIUM STORE DEPLETION.
CC -1- SUBUNIT: ISOFORM ALPHA ASSOCIATES WITH INOSITOL-1,4,5-TRIPHOSPHATE
CC RECEPTOR (ITPR). INTERACTS WITH NHERF (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND
CC BETA/DELTA 514; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ADRENAL GLAND. LOWER EXPRESSION
CC IN HEART AND RETINA. ALSO EXPRESSED IN TESTIS. THE SHORT ISOFORM
CC IS SPECIFICALLY EXPRESSED IN THE ADRENAL GLAND.
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
-----
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X99792; CAA68125.1; -
CC EMBL: AJ224862; CAA12161.1; -
CC InterPro: IPR002110; ANK.
CC InterPro: IPR002111; Cat_channel_TrpL.
CC InterPro: IPR000636; M+channel_nlg
CC InterPro: IPR002153; Trans_recep.
CC

```

DR InterPro: IPR004729; Trp-CaChannel.  
DR Pfam: PF00023; ank; 2.  
DR Pfam: PF00520; Ion\_trans; 1.  
DR PRINTS: PR01097; TRNSRECEPTR.  
DR SMART: SM00248; ANK; 2.  
DR TIGRFAMs: TIGR00870; trp; 1.  
DR PROSITE: PS50088; ANK\_REPEAT; 1.  
DR PROSITE: PS50297; ANK\_REPEAT; 1.  
KW Ionic channel; Transmembrane; Ion transport; Calcium channel;  
KW ANK repeat; Repeat; Alternative splicing.  
FT DOMAIN 1 331 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 332 352 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 353 364 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 365 385 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 386 438 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 439 459 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 460 471 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 472 492 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 493 513 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 514 534 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 535 601 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 602 622 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 623 981 ANK 1.  
FT REPEAT 71 100 ANK 2.  
FT REPEAT 143 172 BINDS TO ITPR1, ITPR2 AND ITPR3 (BY  
FT DOMAIN 617 981 SIMILARITY).  
FT SITE 979 981 ESSENTIAL FOR BINDING TO NHERF PDZ DOMAIN  
FT VARSPLIC 1 513 MISSING (IN ISOFORM BETA).  
FT SEQUENCE 981 AA; 112531 MW; 57B172FD65B791C9 CRC64;  
Query Match  
Best Local Similarity 13.7%; Score 166; DB 1; Length 981;  
Matches 139; Conservative 102; Mismatches 203; Indels 262; Gaps 34;  
QY 222 NMREF-----INSFPRD-----IYY 236  
DB 2 NMAQYKRNVDYRDIPLIVRAESELSPSEKAYLNAVEKGYASVSKSLEAEIYF 61  
QY 237 R-----GOTALHIAERRCKHYVELLVAQADV-----HA 266  
DB 62 KINICIDPLGRPTALLAIENENLELLELLSFNVYVDALLHAIRKEVGVAVELLNKH 121  
QY 267 QARGRFQPK---DEGYFTFGEI-----PLSLAAGTQPHVNYLFE-----NPHKKA 312  
DB 122 KPSEKQVPPILLDK---QFSEFTPDITPIILAAHTNNVEIILKLVQKGVSVPRPH--- 174  
QY 313 DMRQDSRGNTVLHALVAIADNTRENTKFTVKMYDLLLLKCARLPDSNLEAVLNNDG-L 371  
DB 175 -----EVRCNCVCEVSSDVSLSRHSR-----RLNIYKALASPSLIALSSDPFL 220  
QY 372 SPLMMAAKTGKIGIFQHIIRREVTEDTRHLSRKFQDWAYG-----PVYSLYD 420  
DB 221 TAFQLSWELQELSKVNEFESEYEE-----LSRQCKQFADLLDQTRSSRELEILNYRD 275  
QY 421 LSSL--DTCGEASVLEILV-YNSKIENRHEMLAVEPINELLRKW-----RKFGAV 469  
DB 276 DNSLLEQSGNDLARKLAIKYRQK-----EFVAQPCQQLASRWYDFEPPWRRRHWAV 330  
QY 470 -----SFYINVSYLCAMWIFLTAYY--- 491  
DB 331 KWTCTFVGLLPVFSVCYLIAPKSPGLGFIKPIKFIKHTASYLTFLFLLLLASOHID 390  
QY 492 ---QPLEGTTPPYRTVDYLRLA-----GEVITLTGVLFFFT-----NIKDLFMKKC 537  
DB 391 RSDLNROGPPP---TIVENMILPWLGFTWGEIKOMWGDGLQDYIDHWNLMDVFM--- 443  
QY 538 PGVNSLIDG-SQLLYFI-YSLV-----VTVSAALY-LAGIEAYLAWVVALV 583  
DB 444 ---NSLYLATISKIVAFVYKYSALNPRESMDWHMPTLVAEALFAIANIFSSRLISL--- 497  
QY 584 LGMNALLYFRGLKGTCTYSIMIQKILFKDLFRLLVYLLFMICYASALVSLNPPCANMK 643

DB 498 -----FTANSHL-GPLQISLGRMLL-DILKFLFYCLVLLAFANGLNQLFYFYEETK 547  
QY 644 VCNEDQTNCTVPTSPCRDSETFSTF---LLDLFKLTIGMGDL-----EMLSS 688  
DB 548 GLSCCKGIRCE-----KQNAFSTLFTLOSLSFWSIFGLNLYVTVNVAQHEFTFVGA 600  
QY 589 TKYPVFIILLVTVIILTVFVLLNMLALMGETVGVQVSKSKHTWK 734  
DB 601 TMFG-----TYNVISLVLLNMLIAMMNSYQLIADHADIEMK 638  
RESULT 6  
TRP4\_MOUSE  
ID TRP4\_MOUSE STANDARD; PRT; 974 AA.  
AC Q9QUQ5; Q9QZC0; Q9QUQ9; Q62350;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Short transient receptor potential channel 4 (TrpC4) (Receptor-  
activated cation channel TRP4) (Capacitative calcium entry channel  
Trp4).  
GN TRPC4 OR TRRP4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
[1]  
RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
RC TISSUE=Brain;  
RA Zhu X., Boulay G., Jiang M., Birnbaumer L.;  
"Trp4 is involved in capacitative calcium entry in murine cells."  
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
[2]  
RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
RA Qian F., Philipson L.H.;  
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
[3]  
RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
RC TISSUE=Brain;  
RA Mori Y., Takada N., Okada T., Wakamori M., Imoto K., Wanifuchi H.,  
Oka H., Oba A., Ikenaka K., Kurosaki T.;  
RT "Differential distribution of TRP Ca2+ channel isoforms in mouse  
brain."  
RL NeuroReport 9:507-515(1998).  
[4]  
RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
RX MEDLINE=20545496; PubMed=10980202;  
RA Tang Y., Tang J., Chen Z., Trost C., Flockerzi V., Li M., Ramesh V.,  
Zhu M.X.;  
RT "Association of mammalian trp4 and phospholipase C isozymes with a PDZ  
domain-containing protein, NHERF."  
RL J. Biol. Chem. 275:37559-37564(2000).  
[5]  
RN SEQUENCE OF 505-642 FROM N.A.  
RP TISSUE=Brain;  
RC MEDLINE=96003894; PubMed=7575478;  
RA Petersen C.C.H., Berridge M.J., Borge M.F., Bennett D.L.;  
RT "Putative capacitative calcium entry channels: expression of  
Drosophila trp and evidence for the existence of vertebrate  
homologues."  
RL Biochem. J. 311:41-44(1995).  
[6]  
RN FUNCTION.  
RP MEDLINE=21113116; PubMed=11175743;  
RA Freichel M., Suh S.H., Pfeifer A., Schweig U., Trost C.,  
Weissgerber P., Biel M., Philipp S., Freise D., Droogmans G.,  
Hofmann F., Flockerzi V., Nilius B.;  
RT "Lack of an endothelial store-operated Ca2+ current impairs  
agonist-dependent vasorelaxation in TRP4-/- mice."  
RL Nat. Cell Biol. 3:121-127(2001).  
CC -!- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE



RA Juengling E., Luckhoff A., Putney J.W. Jr.;  
 RT "Cloning and expression of the human transient receptor potential 4  
 RT (TRP4) gene: localization and functional expression of human TRP4 and  
 RT TRP3.";  
 RL Biochem. J. 351:735-746(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA; DELTA AND GAMMA).  
 RC TISSUE=Embryonic kidney;  
 RA MEDLINE=21099836; PubMed=11163362;  
 RX Mery L., Magnino F., Schmidt K., Krause K.-H., Dufour J.-F.;  
 RT "Alternative splice variants of htrp4 differentially interact with the  
 RT C-terminal portion of the inositol 1,4,5-trisphosphate receptors.";  
 RL FEBS Lett. 487:377-383(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
 RX MEDLINE=21671347; PubMed=11713258;  
 RA Schaefer M., Plant T.D., Stresow N., Albrecht N., Schultz G.;  
 RT "Functional differences between TRPC4 splice variants.";  
 RL J. Biol. Chem. 277:3752-3759(2002).  
 RN [4]  
 RP SEQUENCE OF 514-633 FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=96234226; PubMed=8646775;  
 RA Zhu X., Jiang M., Peyton M., Boulay G., Hurst R., Stefani E.,  
 RA Birnbaumer L.;  
 RT "trp, a novel mammalian gene family essential for agonist-activated  
 RT capacitative Ca2+ entry.";  
 RL Cell 85:661-671(1996).  
 CC -1- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE  
 CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A  
 CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR  
 CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN  
 CC SHOWN TO BE CALCIUM-SELECTIVE (BY SIMILARITY). MAY ALSO BE  
 CC ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION.  
 CC -1- SUBUNIT: ISOFORM ALPHA BUT ISOFORM BETA ASSOCIATES WITH INOSITOL-  
 CC 1,4,5-TRIPHOSPHATE RECEPTOR (ITPR). INTERACTS WITH NHERF (BY  
 CC SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -1- ALTERNATIVE PRODUCTS: 4 ISOFORMS; ALPHA (SHOWN HERE), BETA, DELTA  
 CC AND GAMMA; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN PLACENTA. EXPRESSED AT  
 CC LOWER LEVELS IN HEART, PANCREAS, KIDNEY AND BRAIN. ISOFORM ALPHA  
 CC WAS FOUND TO BE THE DOMINANT ISOFORM. ISOFORM BETA WAS NOT  
 CC FOUND IN PANCREAS AND BRAIN.  
 CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.  
 CC  
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 CC  
 DR EMBL: AF063822; AAF22927.1; -  
 DR EMBL: AF063823; AAF22928.1; -  
 DR EMBL: AF063824; AAF22929.1; -  
 DR EMBL: AF063825; AAF22930.1; -  
 DR EMBL: AF175406; AAD51736.1; -  
 DR EMBL: AF421358; AAL24549.1; -  
 DR EMBL: AF421359; AAL24550.1; -  
 DR EMBL: U40983; AAC50630.1; -  
 DR Genew: HGNC:12336; TRPC4.  
 DR MIM: 603651;  
 DR InterPro: IPR002110; ANK.  
 DR InterPro: IPR002111; Cat\_channel\_TrpL.  
 DR InterPro: IPR000636; M+channel\_nlg.  
 DR InterPro: IPR002153; Trans\_recep.  
 DR InterPro: IPR004729; Trp\_CaChannel.  
 DR Pfam: PF00023; ank; 2.  
 DR Pfam: PF00520; ion\_trans; 1.

DR PRINTS: PRO1097; TRNSRECEPTR.  
 DR SMART; SMO0248; ANK; 2.  
 DR TRGFAMS; TIGR00870; trp; 1.  
 DR PROSITE; PS50088; ANK\_REPEAT; 1.  
 DR PROSITE; PS50297; ANK\_REPEAT; 1.  
 KW Ionic channel; Transmembrane; Ion transport; Calcium channel;  
 KW ANK repeat; Repeat; Alternative splicing.  
 FT DOMAIN 1 329 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 330 350 POTENTIAL.  
 FT DOMAIN 351 362 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 363 383 POTENTIAL.  
 FT DOMAIN 384 436 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 437 457 POTENTIAL.  
 FT DOMAIN 458 469 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 470 490 POTENTIAL.  
 FT DOMAIN 491 511 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 512 532 POTENTIAL.  
 FT DOMAIN 533 599 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 600 620 POTENTIAL.  
 FT DOMAIN 621 977 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 69 98 ANK 1.  
 FT REPEAT 141 170 ANK 2.  
 FT DOMAIN 377 382 POLY-LEU.  
 FT DOMAIN 615 977 BINDS TO ITPR1, ITPR2 AND ITPR3.  
 FT SITE 972 977 ESSENTIAL FOR BINDING TO NHERF PDZ DOMAIN  
 FT VARSPLIC 629 693 MISSING (IN ISOFORM GAMMA).  
 FT VARSPLIC 730 870 MISSING (IN ISOFORM DELTA).  
 FT VARSPLIC 785 868 MISSING (IN ISOFORM BETA AND ISOFORM  
 FT GAMMA).  
 SQ SEQUENCE 977 AA; 112100 MW; 77E4D27C374D660E CRC64;  
 Query Match 3.6%; Score 164; DB 1; Length 977;  
 Best Local Similarity 20.4%; Pred. No. 0.005;  
 Matches 143; Conservative 103; Mismatches 214; Indels 242; Gaps 34;  
 QY 201 NLSNGRNDIPVLLDIAER--TGNRMREFNSPPR-----DIYR----- 237  
 DB 9 NVNAPRYDRIPLRVRAESELSPKSEKAYLNAVEKGDYASYVKKSLSEAEIYKINICIDP 68  
 QY 238 -GOTALHIAIERCKHYVELLVAOGADV-----HAQARGFFOP 275  
 DB 69 LGRTALLIAIENENLEIELLSFNVYVGDALLHAIRKEVGVGAVELLNHHKPSGKQVP 128  
 QY 276 K--DEGGYFYFGEI-----PLSLAACTNQPHIVNYLTE-----NPHKKADMRRODSRG 321  
 DB 129 PILLDK---QFSEFTDITPILAAHTNNYEIILKLVQGVSVPRPH-----EVRC 176  
 QY 322 NTVLHALVAIADNTRNTKVTMYDILLKCARLPDPSNLEAVLNNDG-LSPMLMAAKT 380  
 DB 177 NCVECVSSSDVDSLRHSR-----RLNIYKALASPSLIALSSEDPFLTAFOLSWEL 227  
 QY 381 KGIGIFQHIIRREVTDTRHLRSKFKDWAYGPVSSLYDLSLDCTCGEASVLEILVY- 439  
 DB 228 QELSKVENEKSEYEE-----LSRQCKQFA-----KDL-LDQTRSRELEIILNR 272  
 QY 440 --NSKIE-----NRHEMLAVEPIFELLRDKW-----RKFAGV----- 469  
 DB 273 DONSLIEQSGNDLARKLAIKYRQKEFVAQPCQQLASRWYDEFPGRWRHWAVMKMT 332  
 QY 470 -----SFYINVSVYLCAMVIFTLTAY-----Q 492  
 DB 333 CFTIGLLFFVESVCYLIAPKSPGLFIRKPFKIFCTASYLTFTLELLLASOHIDRSDL 392  
 QY 493 PLEGTPPYRTTVDYLRLA-----GEVITLFTGVLFFFT-----NIKDLFMKKCPGVN 541  
 DB 393 NRQGGPP-----TIVEMWILPWLVGFINGEIKQMDGLODYIHDWNLDVFM-----N 442  
 QY 542 SLFIDG-SFOLLYFI-YSVL-----VIVSAALY-LAGIEAYLAWFALVGLWM 587  
 DB 443 SLYLATISLKIIVAFVKYSALNPRESMDMHPHTLVAEALFAIANIFFSLRLSL----- 495  
 QY 588 NALYFTRGLKLTGTYSIMIQIKILFKDLFRFLLYVILFMIGYASALVSLNLPNCANKVCNE 647

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Db 496 ----FTANSHL-GPQISLGRMLL-DILKFLFIYCLVLLAFANGNLQY-----FYFE 542
Qy 648 DOTNCTVTPYSCRDSEFTSF---LLDLKFLITIGMDL-----EMLSSKYP 692
Db 543 ETGKLTGKIGRCEKQNAFSLFETLQSLFWSIFGLINLYTNVKAHQEFTEFGATMG 602
Qy 693 VVFILLVYIILFTVLLNNMLIAMGETVQGVSKESKHIMK 734
Db 603 -----TYNVISLVLLNNMLIAMMNSYLIADHADIEWK 636

RESULT 8
TRP4_RAT
ID TRP4_RAT STANDARD: PRT; 977 AA.
AC O35119; Q9EQ75; Q9EQ74;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Short transient receptor potential channel 4 (TrpC4) (Trp4)
DE (Capacitative calcium entry channel 1) (CCE1).
GN TRPC4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC STRAIN=Wistar Inamichi; TISSUE=Brain;
RA MEDLINE=97189270; PubMed=9037541;
RX Funayama M., Goto K., Kondo H.;
RT "Cloning and expression localization of cDNA for rat homolog of TRP
RL protein, a possible store-operated calcium (Ca2+) channel.";
RN Brain Res. Mol. Brain Res. 43:259-266(1996).
[2]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC STRAIN=Sprague-Dawley;
RX MEDLINE=20545496; PubMed=10980202;
RA Tang Y., Tang J., Chen Z., Trost C., Flockerzi V., Li M., Ramesh V.,
RA Zhu M.X.;
RT "Association of mammalian Trp4 and phospholipase C isozymes with a PDZ
RL domain-containing protein, NHERF.";
RL J. Biol. Chem. 275:37559-37564(2000).
CC -1- FUNCTION: THOUGHT TO FORM NON-SELECTIVE A RECEPTOR-ACTIVATED
CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A
CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR
CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN
CC SHOWN TO BE CALCIUM-SELECTIVE (BY SIMILARITY). MAY ALSO BE
CC ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION.
CC -1- SUBUNIT: ISOFORM ALPHA BUT NOT ISOFORM BETA ASSOCIATES WITH
CC INOSITOL-1,4,5-TRIPHOSPHATE RECEPTOR (ITPR). INTERACTS WITH NHERF
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
CC -----
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CC -----
CC EMBL; AF008889; BAA23599.1;
CC EMBL; AF288407; AAC21809.1;
CC EMBL; AF288408; AAC21810.1;
CC InterPro; IPR002110; ANK.
CC InterPro; IPR002111; Cat_channel_TrpL.
CC InterPro; IPR000636; M+channel_nlg.

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DR InterPro; IPR002153; Trans_recep.
DR InterPro; IPR004729; Trp_CaChannel.
DR Pfam; PF00023; ank. 2.
DR Pfam; PF00520; ion_trans. 1.
DR PRINTS; PR01097; TRNSRECEPTR.
DR SMART; SMO0248; ANK. 2.
DR TIGRFAMS; TIGR00870; trp. 1.
DR PROSITE; PS50088; ANK_REPEAT. 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION. 1.
DR Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW ANK repeat; Repeat; Alternative splicing.
FT DOMAIN 1 329 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 330 350 POTENTIAL.
FT DOMAIN 351 362 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 363 383 POTENTIAL.
FT DOMAIN 384 436 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 437 457 POTENTIAL.
FT DOMAIN 458 469 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 470 490 POTENTIAL.
FT DOMAIN 491 511 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 512 532 POTENTIAL.
FT DOMAIN 533 599 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 600 620 POTENTIAL.
FT DOMAIN 621 974 CYTOPLASMIC (POTENTIAL).
FT REPEAT 69 98 ANK 1.
FT REPEAT 141 170 ANK 2.
FT DOMAIN 615 977 BINDS TO ITPR1, ITPR2 AND ITPR3 (BY
FT SIMILARITY).
FT SITE 975 977 ESSENTIAL FOR BINDING TO NHERF PDZ DOMAIN
FT VARSPLIC 784 867 MISSING (IN ISOFORM BETA).
FT CONFLICT 11 11 N -> D (IN REF. 1).
FT CONFLICT 72 76 TALLI -> GLLFSL (IN REF. 1).
FT CONFLICT 121 135 PSGEKQVPPILLDKQ -> AQREAGASHPPWQT (IN
FT REF. 1).
FT CONFLICT 204 204 A -> G (IN REF. 1).
FT CONFLICT 385 411 QHIDRSLNRGGPPPTIVEMWMLPVL -> STST (IN
FT REF. 1).
FT CONFLICT 681 681 K -> M (IN REF. 1).
FT CONFLICT 705 705 Q -> H (IN REF. 1).
FT CONFLICT 728 728 E -> D (IN REF. 1).
FT CONFLICT 807 807 A -> V (IN REF. 1).
FT CONFLICT 873 873 Q -> R (IN REF. 1).
FT CONFLICT 888 888 K -> Q (IN REF. 1).
FT CONFLICT 922 977 VGRKSCSFKEKVVVEDVTPIPKHKAQEDSSIDYDLS
FT PTTVAHEDYVTRFL -> GRQESVLLQVGGGGWEDNR
FT YYTKRNTPRGDSKHKIMI (IN REF. 1).
SQ SEQUENCE 977 AA; 111847 MW; 6F86DA95261E0ECD CRC64;

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Query Match 3.5%; Score 161; DB 1; Length 977;  
 Best Local Similarity 20.6%; Pred. No. 0.0079;  
 Matches 143; Conservative 104; Mismatches 220; Indels 228; Gaps 34;

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Qy 201 NLSGRNDTIPVLLDIAER--TGNMREFINSFPR-----DIYR----- 237
Db 9 NVNAPYDRIPRLIVRAESELSPSEKAYLNAVEKGDYKVSKEAEIVFKINICIDP 68
Qy 238 -GOTALHIAIERCKHYVELLVAGADV-----HAQARGRFQP 275
Db 69 LGRTALLIATENLELLELLSFNVYVGDALLHAIKRVGVAVELLNHHKPSGEQVP 128
Qy 276 K---DEGGYVFYFCEL-----PLSLAACTNPHIVNYLTE-----NPHKADMRRDSRG 321
Db 129 PILLDK---QFSEFTPDTPPIIAHTNNYEIKLLVQKGVSPRRH-----EVRC 176
Qy 322 NTVLHALVAIADTNTRENTKVTKMYDILLKLCARLFPDSNLEAVLNNDG--LSPLMAAKT 380
Db 177 NCVECVSSSDVSDLSRHS-----RLNIYKALASPSLIALSSSEDPeltaFQLSWEL 227
Qy 381 GKIGIFQHIIRREVTDEDTLHLSRKFKDWAYGPVYSSLYDLSLDTGCGEASVLEILVY- 439
Db 228 QELSKVENEKFEVEE-----LSRQCKQFA-----KDL--LDOTRSSRELEIILNRY 272

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QY 440 --NSKIE-----NPHEMLAVEPINELLRDKW-----RKFGAV-----469  
 Db 273 DONSLEBQSGNDLRLAIAIKYRQKEFVAQPCOQLASRYDEFPGRRRHNAVKMYT 332  
 QY 470 -----SFINVSVYLCAMVITLTAY-----Q 492  
 Db 333 CFIIIGLLPVPVSVYLIAPKPLGLFIRKPIKFKICHFTASVLTFLFLLLLASQHIDRSDL 392  
 QY 493 PLEGTTPPYRTVDYURLA-----GEVITLFTGVLFFFT-----NTKDLFMKKCPGVN 541  
 Db 393 NRQGGPPP-----TIVEMILPWLGVINGEIKOMDGGQLQDIHOWNLMDVFM-----N 442  
 QY 542 SLFIDG-SFQLLYFI-YSVL-----VIYSAALY-LAGTAYLAVVAVFALVLCWM 587  
 Db 443 SLIATLSLKIVATVKVSALNPRSDWMHPTLVAEALFAIANFSSURLISL-----495  
 QY 588 NALVFTGRLKLTGYYSIMIOIKFLDKLFRFLVLLVFMIGVASALVSLNPNCAKMKVCNE 647  
 Db 496 ----FTANSHL-GPLQISLGRMLL-DILKFLFIYCLVLLAFANGLNQLFYFEETKGLSC 549  
 QY 648 DOTNCTVPTPSCDSSTFTF---LDDLFLKTGMGDLEMSSTKYPVVF-----IILL 699  
 Db 550 KGIRCE-----KONNAFSTLFTLOSLEWSIFGLINL-VYTNVKAQHETDFVGTATMF 601  
 QY 700 VTYILTFVLLNLMLALMGETVGVQVSKESHK 734  
 Db 602 GTYNVISLVLLNLMLAMNNSYLIADHADIENK 636

RESULT 9  
 TRL2\_HUMAN  
 ID TRL2\_HUMAN STANDARD; PRT: 1503 AA.  
 AC Q94759; Q96KN6;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Long transient receptor potential channel 2 (Ltrpc2) (Transient  
 DE receptor potential channel 7) (Trpc7).  
 GN TRPM2 OR LTRPC2 OR TRPC7 OR KNP3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Brain;  
 RX MEDLINE=99026133; PubMed=9806837;  
 RA Nagamine K., Kudoh J., Minoshima S., Kawasaki K., Asakawa S., Ito F.,  
 RA Shimizu N.;  
 RT "Molecular cloning of a novel putative Ca2+ channel protein (TRPC7)  
 RT highly expressed in brain.";  
 RL Genomics 54:124-131(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RA Wehage E., Elsfield J., Heiner I., Juengling E., Zitt C.,  
 RA Luckhoff A.;  
 RT "Splice variants of LTRPC2 differentially activated by ADP-ribose an  
 RT hydrogen peroxide.";  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20285799; PubMed=10830953;  
 RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,  
 RA Park H.-S., Toyoda A., Ishii K., Tokoi Y., Choi D.-K., Soeda E.,  
 RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,  
 RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,  
 RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,  
 RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,  
 RA Shintani A., Sasaki T., Nagamine K., Mitsuoyama S., Antonarakis S.E.,  
 RA Minoshima S., Shimizu N., Nordstiek G., Hornischer K., Brandt P.,  
 RA Schaefer M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,  
 RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,  
 RA Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,

RA Lehrach H., Reinhardt R., Yaspo M.-L.;  
 RT "The DNA sequence of human chromosome 21.";  
 RL Nature 405:311-319(2000).  
 CC -!- FUNCTION: MAY BE A CALCIUM CHANNEL.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -!- ALTERNATIVE PRODUCTS: At least 2 isoforms; 1 (shown here) and 2;  
 CC are produced by alternative splicing.  
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.  
 CC -!- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. LTRPC  
 CC SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AB001535; BAA34700.1; -;  
 DR EMBL; AJ417076; CAD01139.1; -;  
 DR EMBL; AP001754; BAA95563.1; -;  
 DR Genbank; HGNC:12339; TRPM2.  
 DR MIN; 603749; -;  
 DR InterPro; IPR002111; Cat\_channel\_TrpL.  
 DR InterPro; IPR000636; M-channel\_nlg.  
 DR InterPro; IPR002153; Trans\_recep.  
 DR Pfam; PF00520; Ion\_trans; 1.  
 DR PRINTS; PR01097; TRNSRECEPTP.  
 DR KW Ionic channel; Transmembrane; Ion transport; Calcium channel;  
 KW Alternative splicing.  
 FT DOMAIN 1 752 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 753 773 POTENTIAL.  
 FT DOMAIN 774 795 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 796 816 POTENTIAL.  
 FT DOMAIN 817 820 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 821 841 POTENTIAL.  
 FT DOMAIN 842 896 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 897 917 POTENTIAL.  
 FT DOMAIN 918 936 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 937 957 POTENTIAL.  
 FT DOMAIN 958 1025 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1026 1046 POTENTIAL.  
 FT DOMAIN 1047 1503 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 1504 1503 POTENTIAL.  
 FT VARSPLIC 538 557 MISSING (IN ISOFORM 2).  
 FT VARSPLIC 1291 1325 DTLEPLSTIQYNNVVDGLRRSRFHPYTVQAGLPL -> E  
 FT CONFLICT 1088 1088 S -> N (IN REF. 2).  
 FT CONFLICT 1189 1189 R -> Q (IN REF. 3).  
 FT SEQUENCE 1503 AA; 171225 MW; AD329AE79F1A71B5 CRC64;  
 Query Match 3.4%; Score 155; DB 1; Length 1503;  
 Best Local Similarity 22.4%; Pred. No. 0.035;  
 Matches 72; Conservative 46; Mismatches 98; Indels 106; Gaps 11;  
 QY 469 VSFYINVSVYLCAMVITLTAYVQLEGTPPYRTVDYLR-----AGEVITL-----519  
 Db 797 VVFLNLTSLYFAFLCLF---AYVLMVDVFPVPMSCCAIYLLVLSFVCEEMRQLFYDPDE 853  
 QY 520 -----TGVLFEEFTNIKDLFMKKCPGVNSLFTDGSFQLLYFIYSVLVIVSAALYAGIEAY 574  
 Db 854 CGLMKKAALYF---SDFWNKLDVGAILLFVAG-----LTCRLIPATLYPGRVILS 900  
 QY 575 LAVNVFALVIGWNNALYFTTGLKLTGYYSIMIOIKFLDKLFRFLVLLVFMIGVASALVS 634  
 Db 901 LDFILFCLRLMHFTISKTLGPK-----IIIVKRMKMDVFFFLFLAVVWVSPGVAKQA 954  
 QY 635 LL-----NPKANKVNCNEDQNTCTVPTPS 659  
 Db 955 ILIHNERRVDMVLFPGAYVHSYLTIFGQIPGYIDGVNFPN-----EHCSS---PNTGDPYKPK 1007  
 QY 660 CRSEFTSTFLDLFLKLTICMGDLEMSLSTKYPVVF-----IILLVYIILTFVLLNLML 714













QY 171 FELLTHKKRLDDEE-----PREPSTGKTCLPKALLNLSNRNDTIPVLLDIA 217  
D 63 ---LTHRRQTILREKGRRLANRGPAYMFDNDHSTLSIEERFLDAVEYGN--IPVWKM 117  
QY 218 ERTGNMREFFSPDIYRGOTALHAIERRCKHYVELLV----- 258  
D 118 ECHSLN--VNC-----VDYMGONALQOLAVANEHEITELLKKENLSRVGDALLAISKG 171  
QY 259 -----AQG---ADVHAQA---RGRFFQPKDEGGYFVFGELPLSLAQTNP 298  
D 172 YVRIVEALNHPSPAEGKRLATSPSOSELOQDDFYAYDEDTREFSHDVTPIILAHCOEY 231  
QY 299 HIVNYL-----TENPH-----KKADMRRDSDRGNT----- 323  
D 232 EIVHTLLRKGAIRPHDHYFCKTECSQOKHDSFSRSRINAYKGLASPAYLSLSSD 291  
QY 324 -VLHAL-----VATADNTRENTK-----FVTKMYDLLLLKCARLPDPSNLEAV 365  
D 292 PVMTALELSNLEAVLANIEREFKNDYKLSQCKQDFVVGLLDL-----CRN---TEEVEAI 344  
QY 366 LNDGSLPLMAAKTKGIF--QHIIIRREYTDTRHLSRKFKDWAYGP-----VYSSL 418  
D 345 LNGD-----AETROPDGRPNLSRLKLAID-----EVKKFVAHPNCCQQLLSIW 390  
QY 419 YDLSLDTGGEASVLEILVYNSKIENRHEMLAV-----EPINELLRDKWRK 465  
D 391 YE--NLSLROOTMAVFLV-----VLAVAIGLPFLALIVWCAPCSKMGKIILPRP 438  
QY 466 FGAYSFYINVSYLCAWFIETAYOPLCTGPPYPTVTTVDYRLAGEVITLTGVLFF 525  
D 439 F--WKFAHAASFFIFIGLLVWNA-ADRFEGTKLLPNETSDNAR-----QLFRMTSC 489  
QY 526 FTNIKDLPMKCPGV-----NSLFDGFSQLLYFIYSVL-----VIVSAALYAGIEAYL- 575  
D 490 FSWMEMLIISWVIGMIAWAEKEIWTQGPKEVLFELWNMLDFGLAIIPAASFIARFMAFW 549  
QY 576 -----AVWVFLVLGWNNA 589  
D 550 ASKAQSIIDANDTLKDTKVTLGNVYNYNARIKWDPDQIISGLYAIYAVLSFSRI 609  
QY 590 LYFTRGLKLTYSIMIOKILFKDLFRFLVYLLFMIGYASALVSLNPNCAVMKVCNEDQ 649  
D 610 AYILPANESFQLOISLGRTV-KDIFKFWFIFVWVAFMIGMFLNYS----- 656  
QY 650 TNCVTVPYPSRDSSTFTF---LLDIFKLTIGMDLEMLSTKYPVVFV-----ILLVT 701  
D 657 -----YVIGAKQNEAFTTVEESPKTLFWAIFGLSEVKS-VINYNHKFIENIGYVLGV 709  
QY 702 YIILTFVLLNMLALMGETVGVQSKESKHIWKLOWAT---TILDIERSFPV----- 750  
D 710 YNVTMVIIVLLNMLIAMINSFQIEDDADVEMKFAKLMFYSFEEGRTLVPVFNLPVSP 769  
QY 751 ---FLKAFRSGEMWTVGKSSDGTDPDRRCWFRVD-EVNSHWNQNLGI--INEDPGKNE 803  
D 770 KSLYLLLLKFKWNCMLIOGQKQ-----FQDAEMKNRNEKKFGISGHEDLSK-- 820  
QY 804 TYQYGFSGHTVGLRLDRRWSSVWPVVE---LNKNSNP 838  
D 821 -----FSLDKQLAHNKSST--RSSEDYHLNSFSNP 850

## RESULT 15

TRP3\_HUMAN  
ID TRP3\_HUMAN STANDARD: PRT; 848 AA.  
AC Q13507; Q00593; Q15660;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE 15-JUN-2002 (Rel. 41, Last annotation update)  
GN Short transient receptor potential channel 3 (TrpC3) (Htrp-3) (Htrp3).  
OS TRPC3 OR TRP3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RC SEQUENCE FROM N.A.  
TI TISSUE=Embryonic kidney;  
RX MEDLINE=96234226; PubMed=8646775;  
RA Zhu X., Jiang M., Peyton M., Boulay G., Hurst R., Stefani E.,  
RA Birnbaumer L.;  
RT "trp, a novel mammalian gene family essential for agonist-activated  
RL capacitative Ca2+ entry.";  
RN Cell 85:661-671(1996).  
RN [2]  
RC SEQUENCE FROM N.A.  
TI MEDLINE=97358541; PubMed=9215637;  
RA Xu X.-Z.S., Li H.-S., Guggino W.B., Montell C.;  
RT "Coassembly of TRP and TRPL produces a distinct store-operated  
RL conductance.";  
RN Cell 89:1155-1164(1997).  
RN [3]  
RC SEQUENCE OF 632-747 FROM N.A.  
TI TISSUE=Fetal brain;  
RX MEDLINE=96003837; PubMed=7568191;  
RA Wes P.D., Chevesich J., Jeromin A., Rosenberg C., Stetten G.,  
RA Montell C.;  
RT "TRPC1, a human homolog of a Drosophila store-operated channel.";  
RN Proc. Natl. Acad. Sci. U.S.A. 92:9652-9656(1995).  
RN [4]  
RC CHARACTERIZATION.  
TI MEDLINE=98204851; PubMed=9535843;  
RA Vannier B., Zhu X., Brown D., Birnbaumer L.;  
RT "The membrane topology of human transient receptor potential 3 as  
RL inferred from glycosylation-scanning mutagenesis and epitope  
RN immunocytochemistry.";  
RN J. Biol. Chem. 273:8675-8679(1998).  
RN [5]  
RC FUNCTION.  
TI MEDLINE=98079037; PubMed=9417057;  
RA Zhu X., Jiang M., Birnbaumer L.;  
RT "Receptor-activated Ca2+ influx via human Trp3 stably expressed in  
RN human embryonic kidney (HEK)293 cells. Evidence for a  
RL non-capacitative Ca2+ entry.";  
RN J. Biol. Chem. 273:133-142(1998).  
RN [6]  
RC INTERACTION WITH IP3 RECEPTOR.  
TI MEDLINE=99068646; PubMed=9853757;  
RA Kiselyov K., Xu X., Mozhayeva G., Kuo T., Pessah I., Mignery G.,  
RA Zhu X., Birnbaumer L., Muallem S.;  
RT "Functional interaction between Insp3 receptors and store-operated  
RL Htrp3 channels.";  
RN Nature 396:478-482(1998).  
RN [7]  
RC FUNCTION.  
TI MEDLINE=99127891; PubMed=9930701;  
RA Hofmann T., Obukhov A.G., Schaefer M., Harteneck C., Gudermann T.,  
RA Schultz G.;  
RT "Direct activation of human TRPC6 and TRPC3 channels by  
RL diacylglycerol.";  
RN Nature 397:259-263(1999).  
RN [8]  
RC INTERACTION WITH IP3 RECEPTOR.  
TI MEDLINE=20079588; PubMed=10611319;  
RA Boulay G., Brown D.M., Qin N., Jiang M., Dietrich A., Zhu M.X.,  
RA Chen Z., Birnbaumer M., Mikoshiba K., Birnbaumer L.;  
RT "Modulation of Ca(2+) entry by polypeptides of the inositol 1,4,  
RN 5-trisphosphate receptor (IP3R) that bind transient receptor  
RL potential (TRP): evidence for roles of TRP and IP3R in store  
RT depletion-activated Ca(2+) entry.";  
RN Proc. Natl. Acad. Sci. U.S.A. 96:14955-14960(1999).  
CC -!- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE  
CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A  
CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR  
CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. ACTIVATED BY  
CC DIACYLGLYCEROL (DAG) IN A MEMBRANE-DELIMITED FASHION,

Qy	271	-----RFPQKDEGYFVGELPUSLAACNQPHVNYL-----TENPHK-----A 312
Db	141	ELQDDFYAYDEDTRESPTTPIIAAHQCKYEVHMLLMKGARIERHDYFCKGCDCM 200
Qy	313	DMRRDSDRGNT-----VLHAL-----VAIADNTRENTK----- 340
Db	201	EQRHDSFHSRINAYKGLASPAYLSLSEDDPVLTALSLNELAKLANIEKFNDR 260
Qy	341	-----FVTKWYDLLLKKCARLPDPSNLEAVLNND--GLSPILMAAKTKGIGIFHII 390
Db	261	KLSMOCKDFVGVGLDL-----CR--DSEEEVAILNGDLESAEPLEVHRHKASLSRVKLAI 313
Qy	391	REVTDTRHLRSKFKDWAGPYVSSLYDL--SSLDTCGEASLELLELVYNSKIENRHE 448
Db	314	KYEV-----KKFV--AHPCNQOQLLTWYENJSLREQTIAKCLV----- 352
Qy	449	MLAV-----EPINELLDRKWRKF--GAVSFYINVVSYLCAMVIFTLAY 490
Db	353	VLVVALGFLPFLAIGYWIAPCSRLGKIURSPFMFVAHAASFII-----FLGLVFNASDR 407

QY	491	YQPLEGTPPYRPTVDYLRLAGEV-ITLETGV-LFFFTNIKDLFMKKCPGVNSLFIDGS	548
Db	408	F---EGITLBNITVDYPOIFRKVTQTWTWELIMVVLGMWNSEC--KEWLLEGP	461
QY	549	FOLLYFIYSVL-----VIVSA--ALYLAGTEAYLA-----	576
Db	462	REYILQLANVLDFCMGLSIFAATFARFLAQATKAQQYVDSYVESDISEVTLPEIQY	521
QY	577	-----VMVFALVLGMWNALYFRUGLKLTCTYSIMIOKLFXDLPRF	617
Db	522	FTYARDKWLPDPQIISSEGLYAIAVAFSFSRIAIFYILPANESGPLQIISLGRTV-KDIFKF	580
QY	618	LLVLLFMIGYASALVSLINPCANNKYVCNEDQINCTVPYIPSCRDSETETSTFLLDLFLKT	677
Db	581	MVLFITMVFAPMGIFILSYSLGAKV-----NAAFTTV-----BESEKTLFWISFIGLS	629
QY	678	IMGDMLEMLST-KYPVVVF-----ILLVTYIITLFLINLMIALMGTSVGVSKEKH	731
Db	630	-----EYTSVVLKYDKHFIENICYGVLYGIYNVTMVVLLNLMIAMINSYQOIEDSDSV	683
QY	732	TWK	734
Db	684	EWK	686

Search completed: June 3, 2003, 19:54:43  
Job time : 20 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 3, 2003, 19:49:48 ; Search time 72 Seconds  
(without alignments)

1610.112 Million cell updates/sec

Title: US-09-870-090A-2

Perfect score: 4577

Sequence: 1 MADSEGPACGEVAELPG.....PRCDGHQGYPRKWRDTDDAP 870

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.\*  
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.\*  
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12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*  
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.\*  
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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	4577	100.0	871	22	AAG65787		Human ion channel
2	4577	100.0	871	22	AAE01227		Human vanilloid re
3	4577	100.0	871	23	ABB79191		Human VR4 protein
4	4577	100.0	871	23	AAU74935		Amino acid sequenc
5	4571	99.9	871	22	AAE06681		Human vanilloid re
6	4558	99.6	963	21	AAV96479		Human vanilloid re
7	4558	99.6	963	23	AAU95381		Human calcium tran
8	4546	99.3	871	22	AAG67210		Amino acid sequenc
9	4387	95.8	871	22	AAB86980		Murine ORP4 prot
10	4374	95.6	871	22	AAG67209		Amino acid sequenc

11	4218	92.2	811	22	AAE06682		Human vanilloid re
12	4215	92.1	803	22	AAG63208		Amino acid sequenc
13	3868	84.5	743	22	AAG63209		Amino acid sequenc
14	3829	83.7	742	22	AAE06683		Human vanilloid re
15	3121.5	68.2	602	23	AAE074936		Amino acid sequenc
16	2898.5	63.3	559	23	AAE16773		Human transporter
17	2547	55.6	498	22	AAE04889		Novel human diagno
18	2315.5	50.6	1115	22	ABG28242		Chicken capsaicin
19	1845.5	40.3	843	20	AAV06561		Human vanilloid re
20	1842.5	40.3	843	20	AAW99799		Human vanilloid re
21	1818	39.7	838	20	AAV06555		Rat capsaicin rece
22	1818	39.7	838	20	AAW99789		Rat VR1 capsaicin
23	1818	39.7	838	22	AAE01228		Rattus vanilloid r
24	1801	39.3	839	21	AAV97357		Human VR-1 protein
25	1801	39.3	839	22	AAE01229		Human vanilloid re
26	1800	39.3	839	20	AAV30155		A human vanilloid
27	1800	39.3	839	20	AAV06558		Human capsaicin re
28	1800	39.3	839	21	AAV30152		Human vanilloid re
29	1796	39.2	839	20	AAV30152		A human vanilloid
30	1796	39.2	839	20	AAV30153		A partial human va
31	1795	39.2	839	21	AAV96478		Human vanilloid re
32	1497.5	32.7	761	20	AAV06556		Rat vanilloid rece
33	1497.5	32.7	761	20	AAW99790		Rat VRP-1 (VR2) c
34	1472.5	32.2	763	20	AAV42308		Human vanilloid re
35	1472.5	32.2	763	20	AAV29471		Human vanilloid re
36	1468	32.1	764	22	AAE04890		Human transporter
37	1467	32.1	764	20	AAV29469		Human vanilloid re
38	1467	32.1	764	20	AAV06559		Human vanilloid re
39	1467	32.1	764	21	AAV97358		Human VR-2 protein
40	1467	32.1	764	22	AAV35622		Human vanilloid re
41	1467	32.1	764	23	ABB07817		Human vanilloid re
42	1467	32.1	764	23	AAV51859		Human vanilloid re
43	1464	32.0	764	22	AAE01230		Human vanilloid re
44	1456.5	31.8	764	21	AAV84834		Amino acid sequenc
45	1454.5	31.8	764	23	ABB07818		Human vanilloid re

#### ALIGNMENTS

RESULT 1  
AAG65787  
ID AAG65787 standard; Protein; 871 AA.  
XX  
AC AAG65787;  
XX  
DT 30-JAN-2002 (first entry)  
XX Human ion channel VR-5 protein sequence.  
DE  
XX  
XX Ion channel; vanilloid receptor; VR-3; VR-5; nootropic; neuroprotective;  
KW antiparkinsonian; analgesic; antidiabetic; antiproliferative; cytostatic;  
KW antirheumatic; antiarthritic; gene therapy; antisense therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200168857-A2,  
XX  
PD 20-SEP-2001.  
XX  
PF 15-MAR-2001; 2001WO-US08329.  
XX  
PR 15-MAR-2000; 2000US-0525420.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Curtis RAJ, Cook WJ;  
XX  
DR WPI; 2001-596911/67.  
DR N-PSDB; AAI66972, AAI66973.  
XX  
XX Nucleic acid encoding human ion channels referred to as Vanilloid  
PT receptor 3 (VR-3) and VR-5, useful for screening modulators of VR-3 or

PT VR-5 and for treating calcium homeostasis related disorders (e.g.  
PT dementia) and pain disorders -  
PS Claim 13; Fig 2A-C; 167pp; English.  
XX The invention provides nucleic acid encoding human ion channels referred  
CC to as vanilloid receptor 3 (VR-3) and VR-5. The VR-3 or VR-5 proteins can  
CC be used to screen for naturally occurring VR-3 or VR-5 ligands or for  
CC drugs or compound which modulate VR-3 or VR-5 activity. The VR-3 or VR-5  
CC proteins and their modulators (e.g. antisense nucleic acids and anti-VR  
CC antibodies) are useful for treating disorders characterized by  
CC insufficient or excessive production of VR-3 or VR-5. These disorders are  
CC calcium homeostasis related disorders (Alzheimer's disease, dementia,  
CC Parkinson's disease), pain disorders (diabetic neuropathy, rheumatoid  
CC arthritis) and/or cellular growth and/or proliferation disorders (e.g.  
CC cancer). Numerous other examples of these disorders are given in the  
CC specification. The present sequence represents the human VR-5.  
XX Sequence 871 AA;  
SQ

Query Match 100.0%; Score 4577; DB 22; Length 871;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSEGPAGGVAELPDGSETPGGEAPPLSSANLNFEGEDGSLSPADASRPAGP 60  
DB 1 MADSEGPAGGVAELPDGSETPGGEAPPLSSANLNFEGEDGSLSPADASRPAGP 60  
QY 61 GDGRPNLRMKFQGAFRGVNPIIDLLSTLVSSVPGPKAPMDSLFDYGYRHHSSDN 120  
DB 61 GDGRPNLRMKFQGAFRGVNPIIDLLSTLVSSVPGPKAPMDSLFDYGYRHHSSDN 120  
QY 121 KRRKKIIEKQSPKAPAPQPPILKVFNRPIEDIVSRGSTADLDGLLFLTHKKRL 180  
DB 121 KRRKKIIEKQSPKAPAPQPPILKVFNRPIEDIVSRGSTADLDGLLFLTHKKRL 180  
QY 181 TDEFRPSTGKTCPLKALLNLSNGRNDTIPVLIDIAERTGNMREFINSPPRDIIYRGQT 240  
DB 181 TDEFRPSTGKTCPLKALLNLSNGRNDTIPVLIDIAERTGNMREFINSPPRDIIYRGQT 240  
QY 241 ALHTAIERRCKHYVELLYVAQADYHAQARGFFQPKDEGGYFEGELPLSLAAGTNPPI 300  
DB 241 ALHTAIERRCKHYVELLYVAQADYHAQARGFFQPKDEGGYFEGELPLSLAAGTNPPI 300  
QY 301 VNYLTENPHKKADMRRODSRGNTVLHALVAIADNTRENTKVTMYDILLKLCARLPDPS 360  
DB 301 VNYLTENPHKKADMRRODSRGNTVLHALVAIADNTRENTKVTMYDILLKLCARLPDPS 360  
QY 361 NLEAVLNDGSLPLMMAAKTKIGIFQHIIRREVTDEDTLHLSRKFQDWAYGPVYSSLYD 420  
DB 361 NLEAVLNDGSLPLMMAAKTKIGIFQHIIRREVTDEDTLHLSRKFQDWAYGPVYSSLYD 420  
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKRKFQDWAYGPVYSSLYC 480  
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKRKFQDWAYGPVYSSLYC 480  
QY 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLEFFFTNIDLFMKKCPGV 540  
DB 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLEFFFTNIDLFMKKCPGV 540  
QY 541 NSLFDGSQLLYFIYSLVTVSAALYLAGIEALVAVFALVGLGWNALYFTRLGLKTG 600  
DB 541 NSLFDGSQLLYFIYSLVTVSAALYLAGIEALVAVFALVGLGWNALYFTRLGLKTG 600  
QY 601 TYSIMQIKILFKDLFRELLVYLLFMIGYASALVSLNPNCAKMKVCNEDQNTCTVPTPSC 660  
DB 601 TYSIMQIKILFKDLFRELLVYLLFMIGYASALVSLNPNCAKMKVCNEDQNTCTVPTPSC 660  
QY 661 RDSFTFTFLDLFKLTIGMDLEMLSTKYPVVFIILLVYIILTFVLLNMLIALMGE 720  
DB 661 RDSFTFTFLDLFKLTIGMDLEMLSTKYPVVFIILLVYIILTFVLLNMLIALMGE 720  
QY 721 TVGQVSKESKHWKQWATLIDIERSPFVFLRAFRSGEMVTYVKSSDGTDPDRWCFRV 780

DB 721 TVGQVSKESKHWKQWATLIDIERSPFVFLRAFRSGEMVTYVKSSDGTDPDRWCFRV 780  
QY 781 DEVNWSHWNQNLGIINEDPGKNEYQYGFSGHTYGRLLRRDRWSSVYPRVVELNKNPNDE 840  
DB 781 DEVNWSHWNQNLGIINEDPGKNEYQYGFSGHTYGRLLRRDRWSSVYPRVVELNKNPNDE 840  
QY 841 VVPLDSMGNPRCDGHOOGYQYPRKWRRTDAP 870  
DB 841 VVPLDSMGNPRCDGHOOGYQYPRKWRRTDAP 870  
RESULT 2  
AAE01227  
ID AAE01227 standard; Protein; 871 AA.  
AC AAE01227;  
XX 31-JUL-2001 (first entry)  
DT Human vanilloid receptor 3 (HVR3) protein.  
DE Human vanilloid receptor 3; VR3; inflammation; arthritis; psoriasis;  
KW wound healing; analgesic; vulnary; antiallergic; gene therapy;  
KW neuropathic pain; rhinitis; pruritus; bladder dysfunction;  
KW cluster headache; capsaicin-sensitive ion channel disorder.  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH 238..269  
FT Domain /label= Ankaryn\_repeat  
FT Domain 284..316  
FT Domain /label= Ankaryn\_repeat  
FT Domain 369..402  
FT Domain /label= Ankaryn\_repeat  
FT Domain 470..491  
FT Domain /label= Transmembrane\_domain  
FT Domain 515..535  
FT Domain /label= Transmembrane\_domain  
FT Domain 551..570  
FT Domain /label= Transmembrane\_domain  
FT Domain 575..593  
FT Domain /label= Transmembrane\_domain  
FT Domain 617..635  
FT Domain /label= Transmembrane\_domain  
FT Region 667..681  
FT Domain /label= Poor\_loop\_region  
FT Domain 693..720  
FT Domain /label= Transmembrane\_domain  
XX WO200134805-A2.  
PN 17-MAY-2001.  
PD 10-NOV-2000; 2000WO-US31077.  
PF 12-NOV-1999; 99US-0438997.  
PR (ABBO ) ABBOTT LAB.  
PA Masters JN, Vos MH;  
XX WPI; 2001-335930/35.  
XX N-PSDB; AAD05107.  
XX Novel human vanilloid receptor gene and encoded polypeptides for  
PT identifying compounds that modulate vanilloid receptors in human  
PT tissues and for treating inflammation, arthritis, psoriasis and wound  
PT healing  
XX  
XX Claim 18; Fig 8; 91pp; English.  
XX

CC The present sequence is human vanilloid receptor 3 (hVR3) protein.  
CC Vanilloid receptor protein and its DNA are useful for identifying  
CC compounds which modulate vanilloid receptors in human tissues, which are  
CC useful for treating various disease states, including neuropathic pain,  
CC inflammation, arthritis, rhinitis, pruritus, bladder dysfunction, cluster  
CC headache, wound healing and psoriasis. Vanilloid receptor DNA is useful  
CC as standard or reagent in diagnostic immunoassays, as targets for  
CC pharmaceutical screening assays and also in gene therapy. Vanilloid  
CC receptor protein is useful for detecting the presence of anti-vanilloid  
CC receptor derived polypeptide in test samples. Vanilloid receptor  
CC antibodies are useful for detecting vanilloid receptor polypeptides, for  
CC screening for diseases or conditions associated with abnormal vanilloid  
CC receptor production, treating disorders involving capsaisin-sensitive  
CC ion channels and as diagnostic markers.  
XX  
SQ

Sequence 871 AA;

Query Match 100.0%; Score 4577; DB 22; Length 871;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSGPRAGCEVAELPDESGTGGEGAPFLSSLANLFEDEGSLSPADASRPAGP 60  
DB 1 MADSSGPRAGCEVAELPDESGTGGEGAPFLSSLANLFEDEGSLSPADASRPAGP 60

QY 61 GDGRPNLRMKFQGAFRKGVNPNIDLLLESTLYESSVVGPKKAPMDSLFYGYTRHSSDN 120  
DB 61 GDGRPNLRMKFQGAFRKGVNPNIDLLLESTLYESSVVGPKKAPMDSLFYGYTRHSSDN 120

QY 121 KRRKKIIEKQSPKAPAPQPPPIIKVFNRPIDFIVSRGSTADLDGLLFFLLTHKKRL 180  
DB 121 KRRKKIIEKQSPKAPAPQPPPIIKVFNRPIDFIVSRGSTADLDGLLFFLLTHKKRL 180

QY 181 TDEEFREPSTGKTLCPKALLNLSNGRNDTIPVLLDJAERTGNMRETNPSFRDIYRGQT 240  
DB 181 TDEEFREPSTGKTLCPKALLNLSNGRNDTIPVLLDJAERTGNMRETNPSFRDIYRGQT 240

QY 241 ALHAIERRCKHYVELLVAGADVHAQAARGFPQKDEGGYFYFGEPLSLAACTNPHI 300  
DB 241 ALHAIERRCKHYVELLVAGADVHAQAARGFPQKDEGGYFYFGEPLSLAACTNPHI 300

QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKVFYTKMYDLLLLKCARLPDS 360  
DB 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKVFYTKMYDLLLLKCARLPDS 360

QY 361 NLEAVLNNDGLSLPMAAATGKIGFQHIIRREVTEDTRHLSRKFKDWAYGVPVSSLYD 420  
DB 361 NLEAVLNNDGLSLPMAAATGKIGFQHIIRREVTEDTRHLSRKFKDWAYGVPVSSLYD 420

QY 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYFVNVYSYLC 480  
DB 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYFVNVYSYLC 480

QY 481 AMVIFLTAYQPLEGTPPYTVDYLRAGEVITLFTGVLFFFFTNTKDLPMKKCPGV 540  
DB 481 AMVIFLTAYQPLEGTPPYTVDYLRAGEVITLFTGVLFFFFTNTKDLPMKKCPGV 540

QY 541 NSLFDIGSFOLLYFIYSVLVISAALYLAGIEAYLAVMVFALVGLGMNALLYFRGLKLTG 600  
DB 541 NSLFDIGSFOLLYFIYSVLVISAALYLAGIEAYLAVMVFALVGLGMNALLYFRGLKLTG 600

QY 601 TYSIMIOKILFKDLFRFLVYLLFMIGYASALVSLNPNCKANMKVCNEDQTNCTVTPSC 660  
DB 601 TYSIMIOKILFKDLFRFLVYLLFMIGYASALVSLNPNCKANMKVCNEDQTNCTVTPSC 660

QY 661 RDSSETSTFLDLFKLTIGMGDLEMLSSSTKYPVFFILLVYIILFVLLNMLIALMGE 720  
DB 661 RDSSETSTFLDLFKLTIGMGDLEMLSSSTKYPVFFILLVYIILFVLLNMLIALMGE 720

QY 721 TVGQVSKESHKHWKLOWATTILDIERSEFPVELRKAFRSGEMVTGKSSDGTDPDRRCFRV 780  
DB 721 TVGQVSKESHKHWKLOWATTILDIERSEFPVELRKAFRSGEMVTGKSSDGTDPDRRCFRV 780

QY 781 DEVNWSHWNQNLGIINEDPKNETYQYGFSTHTVGRUURDRWSSVVRVVELNKNNSPDE 840  
DB 781 DEVNWSHWNQNLGIINEDPKNETYQYGFSTHTVGRUURDRWSSVVRVVELNKNNSPDE 840

QY 841 VVPLDSMGNPRCDGHQOQGYPRKWRRTDAP 870  
DB 841 VVPLDSMGNPRCDGHQOQGYPRKWRRTDAP 870

RESULT 3

ID ABB79191 standard; Protein; 871 AA.

XX AC ABB79191;

XX 07-AUG-2002 (first entry)

XX Human VR4 protein SEQ ID NO:2.

XX Human; VR4; vanilloid 4 receptor; receptor; osteopathic; antirheumatic;  
KW antiarthritic; vulnery; analgesic; gene therapy; cartilage; bone;  
KW larynx; auditory canal; intravertebral disc; ligament; tendon;  
KW joint capsule; bone development disorder; osteoporosis; osteoarthritis;  
KW joint destruction; rheumatoid arthritis.

XX Homo sapiens.

XX WO200234280-A2.

XX 02-MAY-2002.

XX 25-OCT-2001; 2001WO-GB04739.

XX 25-OCT-2000; 2000GB-0026114.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Davis JB, Gunthorpe MJ, Egerton J, Smart D;

XX WPI: 2002-471426/50.

XX N-PSDB; ABN87645.

XX Use of vanilloid 4 receptor polypeptide/polynucleotide, a modulator of  
PT the polypeptide or an antisense polynucleotide to the polynucleotide,  
PT for manufacture of a medicament for treating cartilage and/or bone  
PT diseases

XX Claim 8; Page 22; 30pp; English.

XX The present sequence represents human vanilloid 4 receptor (VR4). VR4  
CC has osteopathic, antirheumatic, antiarthritic, vulnery and analgesic  
CC activities. VR4 proteins and polynucleotide sequences can be used in  
CC modulating VR4 activity, in gene therapy and in antisense gene therapy.  
CC VR4 is useful for the manufacture of a medicament for treating diseases  
CC of cartilage and/or bone, or for the treatment of pain associated with  
CC it, where the disease is one affecting the larynx, auditory canal,  
CC intravertebral discs, ligaments, tendons and joint capsules, or a  
CC disease associated with bone development including osteoporosis, or  
CC diseases involving joint destruction such as rheumatoid arthritis or  
CC osteoarthritis, and the pain is associated with rheumatoid arthritis  
CC or osteoarthritis.

XX Sequence 871 AA;

Query Match 100.0%; Score 4577; DB 23; Length 871;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSGPRAGCEVAELPDESGTGGEGAPFLSSLANLFEDEGSLSPADASRPAGP 60  
DB 1 MADSSGPRAGCEVAELPDESGTGGEGAPFLSSLANLFEDEGSLSPADASRPAGP 60

QY 61 GDGRPNLRMKFQGAFRKGVNPNIDLLLESTLYESSVVGPKKAPMDSLFYGYTRHSSDN 120



Db 61 GGRNLRMKFGAERKGVNPDIDLESTLYESSVPGPKAPMDSLFDYGYRHHSSDN 120  
QY 121 KWRKKIIEKQSPKAPAPPPILKVFNRNRPILFEDIVSRGSDADLGLPFLTHKKRL 180  
Db 121 KWRKKIIEKQSPKAPAPPPILKVFNRNRPILFEDIVSRGSDADLGLPFLTHKKRL 180  
QY 181 TDEEFREPSTGKTCLPKALLNLSGRNDTIPVLLDIAERTGNMREFINSPPRDIIYRGQT 240  
Db 181 TDEEFREPSTGKTCLPKALLNLSGRNDTIPVLLDIAERTGNMREFINSPPRDIIYRGQT 240  
QY 241 ALHIAIERCKHYVELLVAGADVHAQAGRFQPKDEGGYFYGELPLSLAACNPHI 300  
Db 241 ALHIAIERCKHYVELLVAGADVHAQAGRFQPKDEGGYFYGELPLSLAACNPHI 300  
QY 301 VNYLTENPHKKADMRRDQSRGNTVHLVAIAADNTRENTKFTVMYDILLKCARLPDPS 360  
Db 301 VNYLTENPHKKADMRRDQSRGNTVHLVAIAADNTRENTKFTVMYDILLKCARLPDPS 360  
QY 361 NLEAVLNNDGLSPLMAAKTGKIGIFQHIIRREVTDETRHLSRKFCDWAYGPVSSLYD 420  
Db 361 NLEAVLNNDGLSPLMAAKTGKIGIFQHIIRREVTDETRHLSRKFCDWAYGPVSSLYD 420  
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRKWRKFGAVSFVNVSYLC 480  
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRKWRKFGAVSFVNVSYLC 480  
QY 481 AWIIFTLAYYOPLGTPPYRTVDYLRAGEVITLFTGVLFNFKDLMFKKCPGV 540  
Db 481 AWIIFTLAYYOPLGTPPYRTVDYLRAGEVITLFTGVLFNFKDLMFKKCPGV 540  
QY 541 NSLFDIGSFOLLYFYISVIVSAALYLAGIEAVLAVMFALVGLGWMNALYFTRGLKLTG 600  
Db 541 NSLFDIGSFOLLYFYISVIVSAALYLAGIEAVLAVMFALVGLGWMNALYFTRGLKLTG 600  
QY 601 TYSIMQIKLFKDLFRLLVYLLFMIGYASALVSLNPNCAKMKVCNEDOTNCTVPTPSC 660  
Db 601 TYSIMQIKLFKDLFRLLVYLLFMIGYASALVSLNPNCAKMKVCNEDOTNCTVPTPSC 660  
QY 661 RDETFSTFLDLKLTIGMGDLEMLSTKYPVVFIIILLVYIILTFVLLNMLIALMGE 720  
Db 661 RDETFSTFLDLKLTIGMGDLEMLSTKYPVVFIIILLVYIILTFVLLNMLIALMGE 720  
QY 721 TVGVSKESKHIWKLQWATTILDIERSPPVFLRAFRSGEMVTGKSSDGTDDRWCFRV 780  
Db 721 TVGVSKESKHIWKLQWATTILDIERSPPVFLRAFRSGEMVTGKSSDGTDDRWCFRV 780  
QY 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSTYGRLLRRDRWSSVPRVELNKNPNDE 840  
Db 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSTYGRLLRRDRWSSVPRVELNKNPNDE 840  
QY 841 VVPLDSMGNPRCDGHOOGYPRKWRDAD 870  
Db 841 VVPLDSMGNPRCDGHOOGYPRKWRDAD 870

RESULT 4  
AAU74935  
ID AAU74935 standard; Protein: 871 AA.  
XX AC AAU74935;  
XX AC AAU74935;  
XX DT 23-APR-2002 (first entry)  
XX DE Amino acid sequence of human vanilloid receptor-like protein 2a (VRL-2a).  
KW Human; vanilloid receptor-like protein 2a; VRL-2a; hypertension;  
KW ion-channel protein; pain; osteoarthritis; diabetic neuropathy;  
KW neuralgia; nerve injury; neurodegeneration; stroke; inflammation;  
KW asthma; allergy; urogenital disorder; incontinence; hypotension;  
KW perivascular disease; VRL-related disease; receptor.  
XX Homo sapiens.  
OS

XX PN EPI160254-AL.  
XX PD 05-DEC-2001.  
XX PF 25-MAY-2001; 2001EP-0304663.  
XX PR 31-MAY-2000; 2000US-208156P.  
XX PA (PFIZ ) PFIZER INC.  
XX PI Shinjo K, Yabuuchi H;  
XX DR WPI; 2002-084359/12.  
XX DR N-PSDB; ABK14002.  
XX PT New human vanilloid receptor-like proteins, useful for identifying  
XX modulators for e.g. treating pain, also related nucleic acid  
XX  
PS Claim 1; Page 17-18; 32pp; English.  
XX  
CC The present invention relates to a new polypeptide that has a sequence  
CC 871 amino acids (AAU74935) or 602 amino acids (AAU74936) long, or their  
CC variants, as defined in the specification. The polypeptide of the  
CC invention is deduced from a human nucleic acid 2749 base pairs (ABK14002)  
CC or 1900 base pairs (ABK14003) long, or their variants, also defined in  
CC the specification. The polypeptides of the invention, which are human  
CC vanilloid receptor-like (VRL) proteins, are used to identify specific  
CC modulators that are potentially useful for treating pain (of any origin),  
CC osteoarthritis, (diabetic) neuropathy, neuralgia, nerve injury,  
CC neurodegeneration, stroke, inflammation, asthma, allergy, urogenital  
CC disorders, incontinence, hypo- or hyper-tension, and perivascular disease.  
CC The molecules of the invention can also be used to raise specific  
CC antibodies. The nucleic acid that encodes the polypeptide of the  
CC invention is useful for recombinant production of the protein and for  
CC preparing transgenic animal models. The polypeptide, antibody and/or  
CC acid of the invention are also useful as diagnostic agents for  
CC determining (susceptibility to) VRL-related diseases. The present amino  
CC acid sequence represents the human vanilloid receptor-like protein 2a  
CC (VRL-2a) of the invention.  
XX  
SQ Sequence 871 AA;

Query Match 100.0%; Score 4577; DB 23; Length 871;  
Best Local Similarity 100.0%; Pred. NO. 0;  
Matches 870; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MADSEGPAGPGEVAELPGDESGTSGEAFPLSSLANLFEDEGSLSPADASRAGP 60  
Db 1 MADSEGPAGPGEVAELPGDESGTSGEAFPLSSLANLFEDEGSLSPADASRAGP 60  
Qy 61 GDGRPNLRMKFOGAFRKGVPNPIDLESTLYESSVPGPKAPMDSLFDYGYRHHSSDN 120  
Db 61 GDGRPNLRMKFOGAFRKGVPNPIDLESTLYESSVPGPKAPMDSLFDYGYRHHSSDN 120  
Qy 121 KWRKKIIEKQSPKAPAPPPILKVFNRNRPILFEDIVSRGSDADLGLPFLTHKKRL 180  
Db 121 KWRKKIIEKQSPKAPAPPPILKVFNRNRPILFEDIVSRGSDADLGLPFLTHKKRL 180  
Qy 181 TDEEFREPSTGKTCLPKALLNLSGRNDTIPVLLDIAERTGNMREFINSPPRDIIYRGQT 240  
Db 181 TDEEFREPSTGKTCLPKALLNLSGRNDTIPVLLDIAERTGNMREFINSPPRDIIYRGQT 240  
Qy 241 ALHIAIERCKHYVELLVAGADVHAQAGRFQPKDEGGYFYGELPLSLAACNPHI 300  
Db 241 ALHIAIERCKHYVELLVAGADVHAQAGRFQPKDEGGYFYGELPLSLAACNPHI 300  
Qy 301 VNYLTENPHKKADMRRDQSRGNTVHLVAIAADNTRENTKFTVMYDILLKCARLPDPS 360  
Db 301 VNYLTENPHKKADMRRDQSRGNTVHLVAIAADNTRENTKFTVMYDILLKCARLPDPS 360  
Qy 361 NLEAVLNNDGLSPLMAAKTGKIGIFQHIIRREVTDETRHLSRKFCDWAYGPVSSLYD 420  
Db 361 NLEAVLNNDGLSPLMAAKTGKIGIFQHIIRREVTDETRHLSRKFCDWAYGPVSSLYD 420

Db 361 NLEAVLNNDGSLPMAAKTKIGIFQHIIRREVTDETRHLSRKFKDWAYGPIVSYLYD 420  
 Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYIINVSYLC 480  
 Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYIINVSYLC 480  
 Qy 481 AMVIFTLAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFNFKDKMCKPGV 540  
 Db 481 AMVIFTLAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFNFKDKMCKPGV 540  
 Qy 541 NSLFDGSPOLLFIYSVLVISAALYAGIEAYLAVWVFLVGLWGNALYFTFGLKLTG 600  
 Db 541 NSLFDGSPOLLFIYSVLVISAALYAGIEAYLAVWVFLVGLWGNALYFTFGLKLTG 600  
 Qy 601 TYSIMIQILFKDLFRFLVYLLPMIGYASALVSLNPNCKMVCNEDQNTCTVPTPSC 660  
 Db 601 TYSIMIQILFKDLFRFLVYLLPMIGYASALVSLNPNCKMVCNEDQNTCTVPTPSC 660  
 Qy 661 RDSETFTFLDLFKLTIGMDLEMLSTKYPPVFIILLVYIILFTVLLNMLIALMGE 720  
 Db 661 RDSETFTFLDLFKLTIGMDLEMLSTKYPPVFIILLVYIILFTVLLNMLIALMGE 720  
 Qy 721 TVGOVSKESKHINKLOWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRRCFRV 780  
 Db 721 TVGOVSKESKHINKLOWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRRCFRV 780  
 Qy 781 DEVNWSHWNGLIINEDPGKNETYQYGFSTVGRLLRDRWSSVPRVVELNKNPNDE 840  
 Db 781 DEVNWSHWNGLIINEDPGKNETYQYGFSTVGRLLRDRWSSVPRVVELNKNPNDE 840  
 Qy 841 VVPLDSMGNPRCDGHQOGYPRKWRITDAP 870  
 Db 841 VVPLDSMGNPRCDGHQOGYPRKWRITDAP 870

## RESULT 5

AAE06681  
 ID AAE06681 standard; Protein; 871 AA.  
 AC AAE06681;  
 XX AAE06681;  
 DT 16-OCT-2001 (first entry)  
 XX Human vanilloid receptor VR3 isoform, VR3A+B-.  
 XX Human; vanilloid receptor; VR3; inflammatory condition; analgesic;  
 KW intractable pain; postherpetic neuralgia; diabetic neuropathy; asthma;  
 KW postmastectomy pain; complex regional pain syndrome; arthritis;  
 KW rheumatoid arthritis; osteoarthritis; ulcer; neurodegenerative disease;  
 KW chronic obstructive pulmonary disease; irritable bowel syndrome;  
 KW psoriasis; central nervous system disease; CNS; cancer;  
 KW intestinal tract disorder; VR3A+B-.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 PN WO200158945-A1.  
 XX WO200158945-A1.  
 PD 16-AUG-2001.  
 XX 01-FEB-2001; 2001WO-US03456.  
 PF 01-FEB-2001; 2001WO-US03456.  
 XX 08-FEB-2000; 2000US-0500123.  
 PR 08-FEB-2000; 2000US-0500123.  
 XX (ORTH ) ORTHO-MCNEIL PHARM INC.  
 PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
 XX Dublin AE, Huvar A, Glass CA, Erlander MG;  
 PI Dublin AE, Huvar A, Glass CA, Erlander MG;  
 XX WPI: 2001-488969/53.  
 DR N-PSDB; AAD12791.  
 XX New human VR3 receptor useful for the treatment of disorders including  
 PT cancers arthritis and pain -  
 XX

Claim 11; Fig 3; 104pp; English.

The patent relates to human vanilloid receptor VR3 polynucleotide and polypeptide. Three isoforms of VR3 namely VR3A+B-, VR3A-B- and VR3A+B+ have also been disclosed. The VR3 polypeptide is used to identify its modulators which are useful for the treatment of inflammatory conditions and for use as analgesics for intractable pain associated with postherpetic neuralgia, diabetic neuropathy, postmastectomy pain, complex regional pain syndromes, arthritis (e.g. rheumatoid and osteoarthritis), as well as ulcers, neurodegenerative diseases, asthma, chronic obstructive pulmonary disease, irritable bowel syndrome and psoriasis. The VR3 modulators are also useful for treatment of central nervous system (CNS) diseases, diseases of the intestinal tract, abnormal proliferation and cancer. The present sequence is human VR3 receptor isoform, VR3A+B-.

Sequence 871 AA;

Query Match 99.9%; Score 4571; DB 22; Length 871;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 869; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MADSSGPRAGPGEVAELPGDESGTSGEAPPLSSLANLFEDEGSLSPADASRAGP 60  
 Db 1 MADSSGPRAGPGEVAELPGDESGTSGEAPPLSSLANLFEDEGSLSPADASRAGP 60  
 Qy 61 GDGRPNLRMFQGAFAKGVNPNIDLLSTLYESSVPPGPKAPMDSLFDYGTYYRHSSDN 120  
 Db 61 GDGRPNLRMFQGAFAKGVNPNIDLLSTLYESSVPPGPKAPMDSLFDYGTYYRHSSDN 120  
 Qy 121 KRWKKTIEKQSPKAPAPQPPILKVFNRPLFDIVSRGSTADLGLLFLTHKKRL 180  
 Db 121 KRWKKTIEKQSPKAPAPQPPILKVFNRPLFDIVSRGSTADLGLLFLTHKKRL 180  
 Qy 181 TDEEFREPSTGKTCPLKALLNLSGRNDTIPVLDIAERTGNMREFTNSPFRDIYRGQT 240  
 Db 181 TDEEFREPSTGKTCPLKALLNLSGRNDTIPVLDIAERTGNMREFTNSPFRDIYRGQT 240  
 Qy 241 ALHTAIERCKHYVELLVAGADVHAQARGFPQKDEGGYFVFGELPLSLAAGTNP 300  
 Db 241 ALHTAIERCKHYVELLVAGADVHAQARGFPQKDEGGYFVFGELPLSLAAGTNP 300  
 Qy 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIAONTRENTKFTVMYDILLKLCARLPDS 360  
 Db 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIAONTRENTKFTVMYDILLKLCARLPDS 360  
 Qy 361 NLEAVLNNDGSLPMAAKTKIGIFQHIIRREVTDETRHLSRKFKDWAYGPIVSYLYD 420  
 Db 361 NLEAVLNNDGSLPMAAKTKIGIFQHIIRREVTDETRHLSRKFKDWAYGPIVSYLYD 420  
 Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYIINVSYLC 480  
 Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSYIINVSYLC 480  
 Qy 481 AMVIFTLAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFNFKDKMCKPGV 540  
 Db 481 AMVIFTLAYQPLEGTPPYRTTVDYLRAGEVITLFTGVLFNFKDKMCKPGV 540  
 Qy 541 NSLFDGSPOLLFIYSVLVISAALYAGIEAYLAVWVFLVGLWGNALYFTFGLKLTG 600  
 Db 541 NSLFDGSPOLLFIYSVLVISAALYAGIEAYLAVWVFLVGLWGNALYFTFGLKLTG 600  
 Qy 601 TYSIMIQILFKDLFRFLVYLLPMIGYASALVSLNPNCKMVCNEDQNTCTVPTPSC 660  
 Db 601 TYSIMIQILFKDLFRFLVYLLPMIGYASALVSLNPNCKMVCNEDQNTCTVPTPSC 660  
 Qy 661 RDSETFTFLDLFKLTIGMDLEMLSTKYPPVFIILLVYIILFTVLLNMLIALMGE 720  
 Db 661 RDSETFTFLDLFKLTIGMDLEMLSTKYPPVFIILLVYIILFTVLLNMLIALMGE 720  
 Qy 721 TVGOVSKESKHINKLOWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRRCFRV 780  
 Db 721 TVGOVSKESKHINKLOWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDDRRCFRV 780

QY 781 DEVNHNQNLGIINEDPKNETYYGFSHTVGRRLRRDRSSVVRVVELNKNNDPE 840  
DB 781 DEVNHNQNLGIINEDPKNETYYGFSHTVGRRLRRDRSSVVRVVELNKNNDPE 840  
QY 841 VVPLDSMGNPRCDGQGGYPRKWRITDAP 870  
DB 841 VVPLDSMGNPRCDGQGGYPRKWRITDAP 870

RESULT 6  
AAY96479  
ID AAY96479 standard; Protein; 963 AA.  
AC AAY96479;  
XX  
DT 12-SEP-2000 (first entry)  
XX  
DE Human vanilloid receptor 3.  
XX  
KW hVR3; vanilloid receptor; dorsal root ganglia; chromosome 12; capsaicin;  
KW marker D12S1893; nociceptor; calcium; influx; inhibitor;  
KW modulator; analgesic; uterine; anti-rheumatic; anti-arthritic;  
KW neuropathic; cerebroprotective; vasotropic; anti-asthmatic;  
KW anti-inflammatory; anti-migraine.

OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Binding-site 329..361  
FT /label= ankyrin\_binding\_domain  
FT Binding-site 376..408  
FT /label= ankyrin\_binding\_domain  
FT Binding-site 461..493  
FT /label= ankyrin\_binding\_domain  
FT Domain 561..583  
FT /label= transmembrane\_domain  
FT Domain 605..622  
FT /label= transmembrane\_domain  
FT Domain 638..660  
FT /label= transmembrane\_domain  
FT Domain 672..697  
FT /label= transmembrane\_domain  
FT Domain 707..725  
FT /label= transmembrane\_domain  
FT Domain 783..811  
FT /label= transmembrane\_domain

WO200032766-A1.  
XX  
XX 08-JUN-2000.  
XX  
XX 30-NOV-1999; 99WO-EP09284.  
XX  
XX 01-DEC-1998; 98GB-0026359.  
XX  
XX (GLAXO) GLAXO GROUP LTD.  
XX  
XX Delany NS, Sanseau P, Tate SN;  
XX  
XX WPI: 2000-412315/35.  
XX  
XX N-PSDB; AAA29173.

Human vanilloid receptor protein or its variant useful for treating or preventing a disorder responsive to the modulation of hVR activity, such as pain, neuropathies, neuralgia, algosia, neurodegeneration.  
XX  
XX Claim 4; Fig 19; 135pp; English.  
XX  
XX Human VR1 is preferentially expressed in human dorsal root ganglia (DRG) and relative to hVR3 has the highest sequence homology with the rat VR1.  
XX  
XX The hVR3 gene maps to chromosome 17 near markers D12S177E and D12S1893.  
XX  
XX hVR1 is activated by capsaicin, the irritant in hot peppers. VRs are

CC nociceptors, transmitting nociceptive and thermoeptive pain information  
CC back to pain-processing centres in the central nervous system. They are  
CC also sites for the release of pro-inflammatory mediators in the  
CC periphery. Capsaicin induces a flux of cations in DRG. The actions of  
CC capsaicin (excitation/desensitisation) are mediated by VRs. The natural  
CC ligand of the recently identified rat VR1 is unknown. It is possible that  
CC hVR sub-types may provide targets for the development of novel analgesic  
CC agents and agents which may interact with other disorders. hVR is useful  
CC for treatment or prophylaxis of a disorder responsive to the modulation  
CC of hVR activity, e.g. pain, neuropathic pain, inflammatory pain, chronic  
CC pain, post-operative pain, rheumatoid arthritis, stroke, ischaemia,  
CC neuralgia, algosia, neurodegeneration, nerve injury, stroke, asthma,  
CC migraine, irritable bowel syndrome (IBS), a respiratory disorder, chronic  
CC obstructive pulmonary disease (COPD), urological disorder,  
CC neuropathy, incontinence, interstitial cystitis or an inflammatory  
CC disorder in a human patient (claimed).

XX Sequence 963 AA;

Query Match 99.6%; Score 4558; DB 21; Length 963;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 867; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MADSEGPAGGGEVAELPGDESGTPGGEAPLSSLANLFEGEDGSLSPADASRPAGP 60  
DB 93 MADSEGPAGGGEVAELPGDESGTPGGEAPLSSLANLFEGEDGSLSPADASRPAGP 152  
QY 61 GGRPNLRMKFGAFKGPVNPIDLESTLVESVVPKPKAPMDSLFDYGYRHHSSDN 120  
DB 153 GGRPNLRMKFGAFKGPVNPIDLESTLVESVVPKPKAPMDSLFDYGYRHHSSDN 212  
QY 121 KWRKKIIEKQSPKAPAPQPPILKVFNRPIPLDIVSRGSTADLDGLLPLTHKKRL 180  
DB 213 KWRKKIIEKQSPKAPAPQPPILKVFNRPIPLDIVSRGSTADLDGLLPLTHKKRL 272  
QY 181 TDEFPREPSTGKTCPLKALLNLSGRNDTIPVLIDIAERTGNMREFINSPERDIYRGQT 240  
DB 273 TDEFPREPSTGKTCPLKALLNLSGRNDTIPVLIDIAERTGNMREFINSPERDIYRGQT 332  
QY 241 ALHAIERRCKHYVELLVAGQADVHAQARGFFQKDEGGYFYFGEPLSLAECTNPHI 300  
DB 333 ALHAIERRCKHYVELLVAGQADVHAQARGFFQKDEGGYFYFGEPLSLAECTNPHI 392  
QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIDNTRENTKFTVMYDILLKLCARLPDPS 360  
DB 393 VNYLTENPHKKADMRQDSRGNTVLHALVAIDNTRENTKFTVMYDILLKLCARLPDPS 452  
QY 361 NLEAVLNNDGLSPLMMAAKTKIGIFQHIIRREVTDETRHLSRKFKDWAYGPVYSSLYD 420  
DB 453 NLEAVLNNDGLSPLMMAAKTKIGIFQHIIRREVTDETRHLSRKFKDWAYGPVYSSLYD 512  
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFCGAVSFYINVSYLEC 480  
DB 513 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFCGAVSFYINVSYLEC 572  
QY 481 AMVIFTLAYYOQLEGPPYPTVTDYLRAGEVITLFTGVLFEEFTNKLDFMKKCPGV 540  
DB 573 AMVIFTLAYYOQLEGPPYPTVTDYLRAGEVITLFTGVLFEEFTNKLDFMKKCPGV 632  
QY 541 NSLFDGSGFOLLFYFYSVLVIVSAALYLAGIEAVLAVMVFALVLGWMNALYFTRGLKLTG 600  
DB 633 NSLFDGSGFOLLFYFYSVLVIVSAALYLAGIEAVLAVMVFALVLGWMNALYFTRGLKLTG 692  
QY 601 TYSIMIQILFKDLFRFLVLLFMIGYASALVLLNPNCAKMKVCNEDQTNCTVPTPSC 660  
DB 693 TYSIMIQILFKDLFRFLVLLFMIGYASALVLLNPNCAKMKVCNEDQTNCTVPTPSC 752  
QY 661 RDSEFTSFILDLFKLTIGMGDLEMLSTKYPVVFVILLVYIILTFVLLNMLIALMGE 720  
DB 753 RDSEFTSFILDLFKLTIGMGDLEMLSTKYPVVFVILLVYIILTFVLLNMLIALMGE 812  
QY 721 TVGVQSVKSHKHWKLOWATTITLIDTSPFPVFLKRAFRSGEMVTGKSSDGTTPDRRCVFRV 780

Db 813 TVGOVSKESKHIWKLQWATTILDIERSPVFLKAFRSGEMVTVGKSSDGTDDRWCVRV 872  
 Qy 781 DEVNWSHWNQNLGIINEDPKNETYQYGFSTHTVGRLLRRDRWSSVPRVVELNKNPNDE 840  
 Db 873 DEVNWSHWNQNLGIINEDPKNETYQYGFSTHTVGRLLRRDRWSSVPRVVELNKNPNDE 932  
 Qy 841 VVPLDSMGNPRCDGHOQGYPRKWRDTPAD 870  
 Db 933 VVPLDSMGNPRCDGHOQGYPRKWRDTPAD 962

## RESULT 7

AAU95381  
 ID AAU95381 standard; Protein; 963 AA.

XX AAU95381;

DT 02-JUL-2002 (first entry)

XX Human calcium transport protein CatrF2E11.

XX Human; human leukocyte antigen; HLA; immunogen: 83P2H3; CatrF2E11;  
 KW calcium transport protein; cancer; prostate cancer; cytostatic;  
 KW chromosome 7q34; chromosome 12q24.1; T cell; B cell.

XX Homo sapiens.

OS WO200214361-A2.

PN 21-FEB-2002.

XX 17-AUG-2001; 2001WO-US25782.

XX 17-AUG-2000; 2000US-226329P.

PA (AGEN-) AGENSYS INC.

XX Raitano AB, Challita-Eid PM, Paris M, Saffran DC, Afar DEH;

PI Levin E, Hubert RS, Ge W, Jakobovits A;

XX WPI: 2002-269179/31.

DR N-PSDB; ABK67431.

XX Monitoring 83P2H3 gene products for monitoring the presence of cancer  
 PT in a subject, comprises determining the status of 83P2H3 gene products  
 PT in a tissue sample from the subject and comparing it to a normal sample

PS Example 1; Fig 2C-2D; 270pp; English.

XX The invention relates to monitoring 83P2H3 (a calcium transport  
 CC protein whose gene is located on chromosome 7q34) gene products in a  
 CC biological sample from a patient who has or is suspected of having  
 CC cancer (especially prostate cancer), comprises: (a) determining the  
 CC status of 83P2H3 gene products expressed by cells in a tissue sample from  
 CC an individual and (b) comparing the status to the status of 83P2H3 gene  
 CC products in a normal sample. Also included are modulators of 83P2H3  
 CC function or status, generating antibodies/immune response against  
 CC 83P2H3 (or related protein CatrF2E11 whose gene is located on chromosome  
 CC 12q24.1) using identified HLA (human leukocyte antigen) binding  
 CC peptides derived from the protein, delivering a cytotoxic agent to  
 CC a cell expressing 83P2H3 by conjugating the agent to an anti-83P2H3  
 CC antibody, a recombinant protein comprising an antigen-binding region of  
 CC the antibody, a non-human transgenic animal that produces the recombinant  
 CC protein, a hybridoma that produces the recombinant protein, a single-  
 CC chain monoclonal antibody that comprises the variable domains of the  
 CC heavy and light chains of the anti-83P2H3 antibody, a vector comprising a  
 CC polynucleotide that encodes the monoclonal antibody and inducing an  
 CC immune response to a 83P2H3 protein, by providing a 83P2H3-related  
 CC protein that comprises a T cell or B cell epitope, and contacting the  
 CC epitope with an immune system T cell or B cell, respectively. The method  
 CC is useful for monitoring 83P2H3 gene products in a biological sample for  
 CC monitoring the presence of cancer in an individual. The modulator is

CC useful for inhibiting the growth of cancer cells that express 83P2H3, for  
 CC treating cancer and the vector is useful for treating a patient with a  
 CC cancer that expresses 83P2H3. The immunological methods are useful for  
 CC generating an immune response against 83P2H3, and for detecting the  
 CC presence of 83P2H3-related protein or polynucleotide in a biological  
 CC sample from a patient who has or who is suspected of having cancer. The  
 CC antibody is useful in prostate cancer diagnosis, prognosis, imaging  
 CC methodologies and treatment, to detect and quantify 83P2H3 and mutant  
 CC 83P2H3-related proteins, for purifying a 83P2H3-related protein, for  
 CC isolating 83P2H3 homologues/related molecules, and for generating anti-  
 CC idiotype antibodies that mimic the 83P2H3 protein. The present sequence  
 CC is the protein sequence of 83P2H3 or its related protein CatrF2E11.

XX SQ Sequence 963 AA;

Query Match 99.6%; Score 4558; DB 23; Length 963;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 867; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MADSEGP	RAGP	GEVAEL	PGDESGT	PGGEAF	PLSSLANL	PEGEDG	SLSPSPAD	ASR	PAGP	60	
Db	93	MADSEGP	RAGP	GEVAEL	PGDESGT	PGGEAF	PLSSLANL	PEGEDG	SLSPSPAD	ASR	PAGP	152	
Qy	61	GDGRPN	LRMK	FGAF	RKGVNP	IDLL	ESTLY	SSVPGP	KKAPMD	SLFDY	GYTRH	SSDN 120	
Db	153	GDGRPN	LRMK	FGAF	RKGVNP	IDLL	ESTLY	SSVPGP	KKAPMD	SLFDY	GYTRH	SSDN 212	
Qy	121	KWRKKI	IEKQ	POS	KAPAP	PPPI	LKVFN	RPI	LDIV	SRGS	TADL	GLLFFLLTHKKRL 180	
Db	213	KWRKKI	IEKQ	POS	KAPAP	PPPI	LKVFN	RPI	LDIV	SRGS	TADL	GLLFFLLTHKKRL 272	
Qy	181	TDEE	REP	STG	KTCL	PKALLN	LSNG	RNDT	IPV	LDIA	ERTGN	RFINS	PFRIIYRGOT 240
Db	273	TDEE	REP	STG	KTCL	PKALLN	LSNG	RNDT	IPV	LDIA	ERTGN	RFINS	PFRIIYRGOT 332
Qy	241	ALHIA	IER	CKHY	VELL	VAQ	ADV	HAQ	AR	FRFP	QKDE	GGYF	YFEGELPLSLA
Db	333	ALHIA	IER	CKHY	VELL	VAQ	ADV	HAQ	AR	FRFP	QKDE	GGYF	YFEGELPLSLA
Qy	301	VNYLT	ENPH	KKAD	MR	QDS	RGN	TVL	HAL	VAI	AD	TRENT	KYFKYMDLLLLKCARLP
Db	393	VNYLT	ENPH	KKAD	MR	QDS	RGN	TVL	HAL	VAI	AD	TRENT	KYFKYMDLLLLKCARLP
Qy	361	NLEAV	LN	DGL	SL	PL	MA	AKT	GKIG	IFQHI	IR	REV	TDETRHLSRKFKDWAYG
Db	453	NLEAV	LN	DGL	SL	PL	MA	AKT	GKIG	IFQHI	IR	REV	TDETRHLSRKFKDWAYG
Qy	421	LS	SLD	TC	G	BEA	S	V	LEI	L	V	YNS	KTENRHEMLAVEP
Db	513	LS	SLD	TC	G	BEA	S	V	LEI	L	V	YNS	KTENRHEMLAVEP
Qy	481	AM	V	I	F	T	L	T	A	Y	Q	P	L
Db	573	AM	V	I	F	T	L	T	A	Y	Q	P	L
Qy	541	NS	L	F	I	D	G	S	F	Q	L	L	I
Db	633	NS	L	F	I	D	G	S	F	Q	L	L	I
Qy	601	T	S	I	M	I	Q	I	K	L	F	K	D
Db	693	T	S	I	M	I	Q	I	K	L	F	K	D
Qy	661	R	S	E	T	F	S	T	F	L	L	D	L
Db	753	R	S	E	T	F	S	T	F	L	L	D	L
Qy	721	T	V	G	O	V	S	K	E	S	K	H	I
Db	813	T	V	G	O	V	S	K	E	S	K	H	I
Qy	781	D	E	V	N	S	H	W	N	Q	L	I	N

Db 873 DEVNWSHWNQNLGIINEDPGKNETYYQYGFSTVGRLLRRDRWSSVPRVVELNKNNSNPDE 932  
Qy 841 VVPLDSMGNPRCDGHQGGYPRKWRRTDDAP 870  
Db 933 VVPLDSMGNPRCDGHQGGYPRKWRRTDDAP 962

RESULT 8  
AAG67210  
ID AAG67210 standard; Protein; 871 AA.  
XX AAG67210;  
AC AAG67210;  
XX AAG67210;  
DT 13-NOV-2001 (first entry)  
DE Amino acid sequence of a human stimulus-responsive channel protein.  
KW Mechanical stimulus-responsive channel protein; kidney; cation channel;  
KW hypertension; diabetes.  
XX Homo sapiens.  
OS WO200162915-A1.  
PN 30-AUG-2001.  
XX 23-FEB-2001; 2001WO-JP01354.  
XX 25-FEB-2000; 2000JP-0048727.  
XX (SNOW ) SNOW BRAND MILK PROD CO LTD.  
XX Suzuki M, Ishibashi K;  
XX WPI: 2001-550089/61.  
DR N-PSDB; AAG67210.  
XX Human or mouse-derived mechanical stimulus-responsive channel protein,  
PT and encoding gene, for screening cation-channel activity enhancers or  
PT inhibitors, or as diagnostics and treatments for hypertension and  
PT diabetes -  
XX Claim 9; Page 25-28; 35pp; Japanese.  
XX The present sequence represents a mechanical stimulus-responsive channel  
CC protein. The protein is expressed specially in the kidney and  
CC non-selectively incorporates cations into cells respondent to a  
CC mechanical stimulus. The mechanical stimulus-responsive channel protein  
CC polynucleotide and polypeptide are useful in screening cation-channel  
CC activity enhancers or inhibitors, as diagnostics or remedies for  
CC diseases such as hypertension and diabetes, and also in drug development  
CC to provide preventative treatment and remedies for the diseases.  
XX Sequence 871 AA;  
SQ

Query Match 99.3%; Score 4546; DB 22; Length 871;  
Best Local Similarity 99.3%; Pred. No. 0;  
Matches 864; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MADSSGPRAGPGEVAELPGDESGTGGGEAFPLSSLANLFEDEGSLSPADASRPPG 60  
Db 1 MADSSGPRAGPGEVAELPGDESGTGGGEAFPLSSLANLFEDEGSLSPADASRPPG 60  
Qy 61 GDGRPNLRMKFQGAFRKGVNPNIDLLSTLYESSVVPKPKAPMDSLFYGTGRHHSSDN 120  
Db 61 GDGRPNLRMKFQGAFRKGVNPNIDLLSTLYESSVVPKPKAPMDSLFYGTGRHHSSDN 120  
Qy 121 KRWKKTIEKQPSKPAPAPQPPPIKVFNRPILFDIVSRGSTADLGLLPFLTHKKRL 180  
Db 121 KRWKKTIEKQPSKPAPAPQPPPIKVFNRPILFDIVSRGSTADLGLLPFLTHKKRL 180  
Qy 181 TDEEFREPSGKTCPLKALLNLNGRNDTIPVLLDIAERTGNMREFINSFRDIYYRGQT 240

Db 181 TDEEFREPSGKTCPLKALLNLNGRNDTIPVLLDIAERTGNMREFINSFRDIYYRGQT 240  
Qy 241 ALHIAIERRCKHYVELLVAQAGADVHAQARGRFQPKDEGGYFFGELPLSLAACTNPHI 300  
Db 241 ALHIAIERRCKHYVELLVAQAGADVHAQARGRFQPKDEGGYFFGELPLSLAACTNPHI 300  
Qy 301 VNYLTENPHKKADMRRODSRGNTVLHALVAIAADNTRENTKFTVMYDLLLLKCARLPDS 360  
Db 301 VNYLTENPHKKADMRRODSRGNTVLHALVAIAADNTRENTKFTVMYDLLLLKCARLPDS 360  
Qy 361 NLEAVLNNDGLSLPMAAATGKIGFOHIIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420  
Db 361 NLEAVLNNDGLSLPMAAATGKIGFOHIIIRREVTDEDTRHLSRKFKDWAYGPVYSSLYD 420  
Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLDRDKWRKFGAVSYINVSYLEC 480  
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLDRDKWRKFGAVSYINVSYLEC 480  
Qy 481 AMVIFLTAYIQPLEGTPPYRTVDYLRAGEVITLFTGVLFPPFTNFKDLFMKKCPGV 540  
Db 481 AMVIFLTAYIQPLEGTPPYRTVDYLRAGEVITLFTGVLFPPFTNFKDLFMKKCPGV 540  
Qy 541 NSLFDIGSFOLLYFIYSVLVISAALYLAGIEAYLAVMVFALVGMNALLYFTRGLKLTG 600  
Db 541 NSLFDIGSFOLLYFIYSVLVISAALYLAGIEAYLAVMVFALVGMNALLYFTRGLKLTG 600  
Qy 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPNCANMKVCNEDQTNCTVTPVPS 660  
Db 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPNCANMKVCNEDQTNCTVTPVPS 660  
Qy 661 RDSETFTFLDLFKLTIGMGDEMLSSSTKYPVVFILLVYIILFVLLNMLIALMGE 720  
Db 661 RDSETFTFLDLFKLTIGMGDEMLSSSTKYPVVFILLVYIILFVLLNMLIALMGE 720  
Qy 721 TVGQVSKESKHINKLOWATTILDIERSFPVFLKAFRSGBMTVVGKSSDGTDPDRRCFRV 780  
Db 721 TVGQVSKESKHINKLOWATTILDIERSFPVFLKAFRSGBMTVVGKSSDGTDPDRRCFRV 780  
Qy 781 DEYNWSHWNQNLGIINEDPGKNETYYQYGFSTVGRLLRRDRWSSVPRVVELNKNNSNPDE 840  
Db 781 DEYNWSHWNQNLGIINEDPGKNETYYQYGFSTVGRLLRRDRWSSVPRVVELNKNNSNPDE 840  
Qy 841 VVPLDSMGNPRCDGHQGGYPRKWRRTDDAP 870  
Db 841 VVPLDSMGNPRCDGHQGGYPRKWRRTDDAP 870

RESULT 9  
AAB86980  
ID AAB86980 standard; Protein; 871 AA.  
XX AAB86980;  
XX 11-DEC-2001 (first entry)  
DT Murine OTRPC4 protein.  
DE OTRPC4; non-selective cation channel; antidiabetic; antihyperlipemic;  
KW antihyperproteemic; antihypertensive; cerebral; renal; osmolality;  
KW osmo-sensor; diabetes; hyper-lipemia; hyper-proteinemia; hypertension;  
KW stroke; renal insufficiency; shock; hyper-osmolality; hypo-osmolality;  
KW transgenic animal; murine.  
XX Mus sp.  
XX DE10013296-Al.  
PN 20-SEP-2001.  
PD 17-MAR-2000; 2000DE-1013296.  
PF 17-MAR-2000; 2000DE-1013296.  
PR 17-MAR-2000; 2000DE-1013296.  
XX

PA (BOEH ) BOEHRINGER INGELHEIM PHARMA KG.  
 XX Schults G, Plant T, Strotmann R, Harteneck C, Nunnenmacher K;  
 PI WPI: 2001-590742/67.  
 XX N-PSDB; AA168414.  
 DR New nucleic acid encoding the non-selective cation channel OTRPC4,  
 XX useful for treating osmolality-associated disorders, e.g. diabetes  
 PT comprises the modulation of activity -  
 PT  
 XX  
 PS Example 1: Fig 2; 68pp; German.  
 XX  
 CC This invention describes a novel nucleic acid (I) which encodes a  
 CC non-selective cation channel, OTRPC4 or its fragments, functional or  
 CC allelic variants or subunits, variants of (I) within the degeneracy of  
 CC the genetic code. The products of the invention have antidiabetic,  
 CC antihyperlipemic, antihyperproteinemic, antihypertensive, cerebral and  
 CC renal activity and are capable of modulating activity of OTRPC4, a  
 CC non-selective cation channel that is regulated by changes in osmolality  
 CC of the extracellular medium, i.e. it is an osmo-sensor for regulating  
 CC cell volume. OTRPC4 is stimulated by a reduction in osmolality and is  
 CC permeable for all cations, but with a preference for calcium.  
 CC Polypeptides (II), encoded by (I), are useful for identifying  
 CC (ant)agonists or modulators of (II), specifically blockers, activators  
 CC or modulators of OTRPC4. (I) (or derived antisense molecules, vectors,  
 CC and transfected cells) and (II) are useful for treating diabetes,  
 CC hyper-lipemia or hyper-proteinemia, hypertension, stroke, renal  
 CC insufficiency, shock or other pathological conditions associated with  
 CC hyper- or hypo-osmolality. (I) is also used to prepare transgenic animals  
 CC having an added, deleted or modified gene for OTRPC4. This sequence  
 CC represents the murine OTRPC4 cation channel described in the method of  
 CC the invention.  
 XX  
 XX Sequence 871 AA;

Query Match 95.8%; Score 4387; DB 22; Length 871;  
 Best Local Similarity 95.2%; Pred. No. 0;  
 Matches 828; Conservative 20; Mismatches 22; Indels 0; Gaps 0;

QY 1 MADSSGPRAGCEVAELPGDESGTGCGEAFPLSSLANLFEDEGSLSPADASRAGP 60  
 DB 1 MADGDPRAAPEVAEPDESGTSGGEAFPLSSLANLFEDEGSSLSLPVDSRAGP 60  
 QY 61 GDGRPNLRMKFQGAFRGVNPNIDLLSTLYESSVWPGKAPKAPMDSLFDTYGRHSSDN 120  
 DB 61 GDGRPNLRMKFQGAFRGVNPNIDLLSTLYESSVWPGKAPKAPMDSLFDTYGRHSSDN 120  
 QY 121 KWRKKTIEKOPSPKAPAPQPPPIKLVFNRPILFDIVSRGSTADLDGLLFLTHKKRL 180  
 DB 121 KWRKRVKVEKOPSPKAPAPQPPPIKLVFNRPILFDIVSRGSTADLDGLLFLTHKKRL 180  
 QY 181 TDEFRPSTGKTCPLKALLNLNGRNDTIPVLLDIAERTGNRMREFINSFRIYRGQT 240  
 DB 181 TDEFRPSTGKTCPLKALLNLNGRNDTIPVLLDIAERTGNRMREFINSFRIYRGQT 240  
 QY 241 ALHAIATERRCKHVVLLVAQADYHAQARGFRFPQKDEGGYFVFGELPLSLAACTNPHI 300  
 DB 241 SLHAIATERRCKHVVLLVAQADYHAQARGFRFPQKDEGGYFVFGELPLSLAACTNPHI 300  
 QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKCARLPFDS 360  
 DB 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKCARLPFDS 360  
 QY 361 NLEAVLNDGLSLPMAAATGKIGIFQHIIRREVTDTRHLSRKPKDWAYGVPYSSLYD 420  
 DB 361 NLETVLNDGLSLPMAAATGKIGIFQHIIRREVTDTRHLSRKPKDWAYGVPYSSLYD 420  
 QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVPINELLRDKWRKFGAVSFYINVSYLEC 480  
 DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVPINELLRDKWRKFGAVSFYINVSYLEC 480  
 QY 481 AMVIFTLAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFFFTSIKDLFTKKCPGV 540

DB 481 AMVIFTLAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFFFTSIKDLFTKKCPGV 540  
 QY 541 NSLFDGSGFOLLFYIYSVLVYSAAALYAGIEAYLVAVFALVGNWALYFTGRGLKLTG 600  
 DB 541 NSLFDGSGFOLLFYIYSVLVYSAAALYAGIEAYLVAVFALVGNWALYFTGRGLKLTG 600  
 QY 601 TYSIMIQKILFKDLFRFLVLLFMIGYASALVSNPCANMKVCNEDQTNCTVPTYPSC 660  
 DB 601 TYSIMIQKILFKDLFRFLVLLFMIGYASALVSNPCANMKVCNEDQTNCTVPTYPAC 660  
 QY 661 RDSETFSTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIITLVLLNMLIALMGE 720  
 DB 661 RDSETFSAFLDLFKLTIGMDLEMLSSAKYPVVFILLVYIITLVLLNMLIALMGE 720  
 QY 721 TVGOVSKEKHINKLOWATILDIERSFPVFLKAFRSGEMVTVGKSSDGTDPDRRCFRV 780  
 DB 721 TVGOVSKEKHINKLOWATILDIERSFPVFLKAFRSGEMVTVGKSSDGTDPDRRCFRV 780  
 QY 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSTVGRLLRRDRSSVWVPRVVELNKNNSPDE 840  
 DB 781 DEVNWSHWNQNLGIINEDPGKSEIYQYGFSTVGRLLRRDRSSVWVPRVVELNKNSSADE 840  
 QY 841 VVPLDSMGNPRCDGHQOQGYPRKWRDTADP 870  
 DB 841 VVPLDLNLGNPCDGHQOQGYAPKWRDTADP 870

## RESULT 10

AAG67209  
 ID AAG67209 standard; Protein: 871 AA.

XX AC AAG67209;

XX DT 13-NOV-2001 (first entry)

XX DE Amino acid sequence of a murine stimulus-responsive channel protein.

XX KW Mechanical stimulus-responsive channel protein; kidney; cation channel;  
 XX KW hypertension; diabetes.

XX OS Mus sp.

XX PN WO200162915-A1.

XX PD 30-AUG-2001.

XX PF 23-FEB-2001; 2001WO-JP01354.

XX PR 25-FEB-2000; 2000JP-0048727.

XX PA (SNOW ) SNOW BRAND MILK PROD CO LTD.

XX PI Suzuki M, Ishibashi K;

XX DR N-PSDB; AAH75192.

XX PT Human or mouse-derived mechanical stimulus-responsive channel protein,  
 XX PT and encoding gene, for screening cation-channel activity enhancers or  
 XX PT inhibitors, or as diagnostics and treatments for hypertension and  
 XX PT diabetes

XX PS Claim 3; Page 20-23; 35pp; Japanese.

XX CC The present sequence represents a mechanical stimulus-responsive channel  
 CC CC protein. The protein is expressed specially in the kidney and  
 CC CC non-selectively incorporates cations into cells responsive to a  
 CC CC mechanical stimulus. The mechanical stimulus-responsive channel protein  
 CC CC polynucleotide and polypeptide are useful in screening cation-channel  
 CC CC activity enhancers or inhibitors, as diagnostics or remedies for  
 CC CC diseases such as hypertension and diabetes, and also in drug development  
 CC CC to provide preventative treatment and remedies for the diseases.

XX	Sequence	871 AA;	Query Match	95.6%;	Score 4374;	DB 22;	Length 871;	Best Local Similarity	94.8%;	Pred. No. 0;	Mismatches	22;	Conservative	825;	Indels	0;	Gaps	0;
XX	16-OCT-2001 (first entry)																	
XX	Human vanilloid receptor VR3 isoform, VR3A-B-.																	
XX	Human: vanilloid receptor; VR3; inflammatory condition; analgesic;																	
XX	intractable pain; postherpetic neuralgia; diabetic neuropathy; asthma;																	
XX	postmastectomy pain; complex regional pain syndrome; arthritis;																	
XX	rheumatoid arthritis; osteoarthritis; ulcer; neurodegenerative disease;																	
XX	chronic obstructive pulmonary disease; irritable bowel syndrome;																	
XX	psoriasis; central nervous system disease; CNS; cancer;																	
XX	intestinal tract disorder; VR3A-B-.																	
XX	Homo sapiens.																	
XX	WO200158945-A1.																	
XX	16-AUG-2001.																	
XX	01-FEB-2001; 2001WO-US03456.																	
XX	08-FEB-2000; 2000US-0500123.																	
XX	(ORTH ) ORTHO-MCNEIL PHARM INC.																	
XX	Dubin AE, Huvar A, Glass CA, Erlander MG;																	
XX	WPI: 2001-488969/53.																	
XX	N-PSDB: AAD12792.																	
XX	New human VR3 receptor useful for the treatment of disorders including																	
XX	cancers arthritis and pain -																	
XX	Claim 11; Fig 5; 104pp; English.																	
XX	The patent relates to human vanilloid receptor VR3 polynucleotide and																	
XX	polypeptide. Three isoforms of VR3 namely VR3A-B-, VR3A-B- and VR3A-B+																	
XX	have also been disclosed. The VR3 polypeptide is used to identify its																	
XX	modulators which are useful for the treatment of inflammatory conditions																	
XX	and for use as analgesics for intractable pain associated with																	
XX	postherpetic neuralgia, diabetic neuropathy, postmastectomy pain, complex																	
XX	regional pain syndromes, arthritis (e.g. rheumatoid and osteoarthritis),																	
XX	as well as ulcers, neurodegenerative diseases, asthma, chronic																	
XX	obstructive pulmonary disease, irritable bowel syndrome and psoriasis.																	
XX	The VR3 modulators are also useful for treatment of central nervous																	
XX	system (CNS) diseases, diseases of the intestinal tract, abnormal																	
XX	proliferation and cancer. The present sequence is human VR3 receptor																	
XX	isoform, VR3A-B-.																	
XX	Sequence 811 AA;																	
XX	Query Match																	
XX	Best Local Similarity																	
XX	Mismatches																	
XX	Conservative																	
XX	Indels																	
XX	Gaps																	

RESULT 11  
AAE06682 .  
ID    AAE06  
XX  
AC    AAE06

Db 241 ALHAIERRCKHYVELLVAQADVHAQARGFFQPKDEGGYFYGELPLSLAACTNPHI 300  
Qy 301 VNYLTENPHKADMRRODSRGNTVLHALVAADNTRENTKFTKMYDLKLLKCARLPDS 360  
Db 301 VNYLTENPHKADMRRODSRGNTVLHALVAADNTRENTKFTKMYDLKLLKCARLPDS 360  
Qy 361 NLEAVLNDGLSPLMAAKTGKIGIFQHIIRREVTDETRHLSRKFKDWAYGPVYSSLYD 420  
Db 361 NLEAVLNDGLSPLMAAKTG----- 381  
Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYL 480  
Db 382 -----KIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYL 420  
Qy 481 AMVIFLTAYYQLEGPPYRTVDYLRAGEVITLFTGVLFEEFNKIDLFMKKCPGV 540  
Db 421 AMVIFLTAYYQLEGPPYRTVDYLRAGEVITLFTGVLFEEFNKIDLFMKKCPGV 480  
Qy 541 NSLFDGSGFOLLFYIYSVLVSAALYLAGIEAYLAVMVFALVGLGMNLYFTFRLKLTG 600  
Db 481 NSLFDGSGFOLLFYIYSVLVSAALYLAGIEAYLAVMVFALVGLGMNLYFTFRLKLTG 540  
Qy 601 TYSIMIOKILFKDLFRLLVYLLFPMIGYASALVSLNPNCAVMKVCNEDQNTCTVTPSC 660  
Db 541 TYSIMIOKILFKDLFRLLVYLLFPMIGYASALVSLNPNCAVMKVCNEDQNTCTVTPSC 600  
Qy 661 RDSFTFTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILFTVLLNMLIALMGE 720  
Db 601 RDSFTFTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILFTVLLNMLIALMGE 660  
Qy 721 TVGQVSKESHIMKLOWATWILDIERSFPVFLKAFSGEMVTGKSSDGTDPDRMCFV 780  
Db 661 TVGQVSKESHIMKLOWATWILDIERSFPVFLKAFSGEMVTGKSSDGTDPDRMCFV 720  
Qy 781 DEVNWSHWNOLGIINEDPKNETYQYGFSTVGRRLRRDRSSVPRVVELNKNPNDE 840  
Db 721 DEVNWSHWNOLGIINEDPKNETYQYGFSTVGRRLRRDRSSVPRVVELNKNPNDE 780  
Qy 841 VVYPLDSMGNPRCDGHOOGYPRKWRDTDP 870  
Db 781 VVYPLDSMGNPRCDGHOOGYPRKWRDTDP 810

RESULT 12  
AAG63208  
ID AAG63208 standard; Protein; 803 AA.  
XX  
AC AAG63208;  
XX  
DT 01-OCT-2001 (first entry)  
XX  
DE Amino acid sequence of novel human gene hcCh3.1.  
XX  
KW Human; hcCh3.1; hcCh3.2; hcCh4; cation channel; Alzheimer's disease;  
KW ionic homeostatic dysfunction; central nervous system disorder;  
KW stroke; neurological disorder; cardiac disorder; arrhythmia; diabetes;  
KW chronic pain; hypercalcemia; hypocalcemia; hypercalciuria; hypocalciuria;  
KW ion disorder; renal disease; liver disease.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 765  
FT /note= "Asn encoded by AAG"  
XX  
PN W0200153348-A2.  
XX  
PD 26-JUL-2001.  
XX  
PF 19-JAN-2001; 2001WO-US01804.  
XX  
PR 21-JAN-2000; 2000US-0177554.  
XX

PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
PI Gaughan GT, Ramanathan CS;  
XX  
DR WPI; 2001-476103/51.  
DR N-PSDB; AAH42583.  
XX  
PT New human cation channel nucleic acids and polypeptides, useful for  
PT diagnosing and treating cation channel dysfunction, e.g. stroke or  
PT neurological disorders (e.g. Alzheimer's disease), cardiac disorders or  
PT diabetes  
XX  
PS Claim 24; Fig 2; 68pp; English.  
XX  
CC The present sequence represents a novel human polypeptide, designated  
CC hcCh3.1. The specification also describes hcCh3.2 and hcCh4. hcCh are  
CC human cation channels. The hcCh nucleic acid molecules and polypeptides  
CC are useful for diagnosing and treating a variety of human disease  
CC conditions that involve ion, particularly cation, channel dysfunction.  
CC Specifically, the nucleic acids and polypeptides are useful for treating  
CC human diseases, which involve calcium, sodium, potassium or other ionic  
CC homeostatic dysfunction, e.g. central nervous system disorders (e.g.  
CC stroke or neurological disorders such as Alzheimer's disease), cardiac  
CC disorders (e.g. arrhythmia), diabetes, chronic pain, hypercalcemia,  
CC hypocalcemia, hypercalciuria, hypocalciuria, or ion disorders  
CC associated with renal or liver disease. In addition, the nucleic acid  
CC molecules and polypeptides are useful in assays for identifying  
CC compounds that modulate the expression of the hcCh genes and/or  
CC activity of the hcCh gene products.  
XX  
SQ Sequence 803 AA;  
XX  
Query Match 92.1%; Score 4215; DB 22; Length 803;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 801; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 69 MKFGAFKRGKVPNPIDLESTLYESSVVPKAPMDSLFDYGYRHHSSDNKRKKII 128  
Db 1 MKFGAFKRGKVPNPIDLESTLYESSVVPKAPMDSLFDYGYRHHSSDNKRKKII 60  
Qy 129 EKQPSKPAPQPPPIKLVFNRPILFDIVSRSTADLGLLFLTHKKRLDEEPREP 188  
Db 61 EKQPSKPAPQPPPIKLVFNRPILFDIVSRSTADLGLLFLTHKKRLDEEPREP 120  
Qy 189 STGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPRDIYRGQTAHTAIER 248  
Db 121 STGKTCLPKALLNSGRNDTIPVLLDIAERTGNMREFINSPRDIYRGQTAHTAIER 180  
Qy 249 RCHYVELLVAQADVHAQARGFFQPKDEGGYFYGELPLSLAACTNPHIYNYLTENP 308  
Db 181 RCHYVELLVAQADVHAQARGFFQPKDEGGYFYGELPLSLAACTNPHIYNYLTENP 240  
Qy 309 HKKADMRRODSRGNTVLHALVAADNTRENTKFTKMYDLKLLKCARLPDSNLEAVLNN 368  
Db 241 HKKADMRRODSRGNTVLHALVAADNTRENTKFTKMYDLKLLKCARLPDSNLEAVLNN 300  
Qy 369 DGLSPLMMAAKTGKIGIFQHIIRREVTDETRHLSRKFKDWAYGPVYSSLYDSSLDTCG 428  
Db 301 DGLSPLMMAAKTGKIGIFQHIIRREVTDETRHLSRKFKDWAYGPVYSSLYDSSLDTCG 360  
Qy 429 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLCAWIFTLT 488  
Db 361 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLCAWIFTLT 420  
Qy 489 AYYQLEGTPPPYRTVDYLRAGEVITLFTGVLFEEFNKIDLFMKKCPGVNSLIDGS 548  
Db 421 AYYQLEGTPPPYRTVDYLRAGEVITLFTGVLFEEFNKIDLFMKKCPGVNSLIDGS 480  
Qy 549 FOLLYFTYSVLVSAALYLAGIEAYLAVMVFALVGLGMNLYFTFRLKLTGTYSIMIOK 608  
Db 481 FOLLYFTYSVLVSAALYLAGIEAYLAVMVFALVGLGMNLYFTFRLKLTGTYSIMIOK 540  
Qy 609 ILFKDLFRLLVYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVTPVPSRDETST 668



|||||  
541 ILFKDLFRLLVLLFMIGYASALVSLNPNCAKMKVCNEDQNTCTVTPYPSCRDSEFST 600  
669 FLDDLFLKLTIGMDLEMLSSKYPVVFILVYIILTFVLLNMLIALMGSTVGQVSKE 728  
601 FLDDLFLKLTIGMDLEMLSSKYPVVFILVYIILTFVLLNMLIALMGSTVGQVSKE 660  
729 SKHIWKLOWATTILDIERSPVFLKAFRSGEMVTVGKSDGTPDRRCFRVDEVNWSHW 788  
661 SKHIWKLOWATTILDIERSPVFLKAFRSGEMVTVGKSDGTPDRRCFRVDEVNWSHW 720  
789 NONLGIINEDPGKNETYYGFSHTVGRRLDRWSSVPRVVELNKNPNDEVVVPLDSM 848  
721 NONLGIINEDPGKNETYYGFSHTVGRRLDRWSSVPRVVELNKNPNDEVVVPLDSM 780  
849 GNPRCDGHQOQYPRKWRDDAP 870  
781 GNPRCDGHQOQYPRKWRDDAP 802

RESULT 13

AAG63209  
ID AAG63209 standard; Protein: 743 AA.

XX AAG63209;

XX 01-OCT-2001 (first entry)

XX Amino acid sequence of novel human gene hcCh3.2.3.

XX Human; hcCh3.1; hcCh3.2; hcCh4; cation channel; Alzheimer's disease;  
KW ionic homeostatic dysfunction; central nervous system disorder;  
KW stroke; neurological disorder; cardiac disorder; arrhythmia; diabetes;  
KW chronic pain; hypercalcemia; hypocalcemia; hypercalciuria; hypocalciuria;  
KW ion disorder; renal disease; liver disease.

XX Homo sapiens.

XX Key . Location/Qualifiers  
FH Misc-difference 705

FT /note= "Asn encoded by AAG"

PN W0200153348-A2.

XX 26-JUL-2001.

XX 19-JAN-2001; 2001WO-US01804.

XX 21-JAN-2000; 2000US-0177554.

XX (BRIM ) BRISTOL-MYERS SQUIBB CO.

XX Gaughan GT, Ramanathan CS;

XX WPI; 2001-476103/51.

XX N-PSDB; AA42584.

PT New human cation channel nucleic acids and polypeptides, useful for  
PT diagnosing and treating cation channel dysfunction, e.g. stroke or  
PT neurological disorders (e.g. Alzheimer's disease), cardiac disorders or  
PT diabetes

PS Claim 24; Fig 4; 68pp; English.

XX The present sequence represents a novel human polypeptide, designated  
CC hcCh3.2. The specification also describes hcCh3.1 and hcCh4. hcCh are  
CC human cation channels. The hcCh nucleic acid molecules and polypeptides  
CC are useful for diagnosing and treating a variety of human disease  
CC conditions that involve ion, particularly cation, channel dysfunction.  
CC Specifically, the nucleic acids and polypeptides are useful for treating  
CC human diseases, which involve calcium, sodium, potassium or other ionic  
CC homeostatic dysfunction, e.g. central nervous system disorders (e.g.  
CC stroke or neurological disorders such as Alzheimer's disease), cardiac

CC disorders (e.g. arrhythmia), diabetes, chronic pain, hypercalcemia,  
CC hypocalcemia, hypercalciuria, hypocalciuria, or ion disorders  
CC associated with renal or liver disease. In addition, the nucleic acid  
CC molecules and polypeptides are useful in assays for identifying  
CC compounds that modulate the expression of the hcCh genes and/or  
CC activity of the hcCh gene products.

XX Sequence 743 AA;

Query Match 84.5%; Score 3868; DB 22; Length 743;  
Best Local Similarity 92.5%; Pred. No. 0;  
Matches 742; Conservative 0; Mismatches 0; Indels 60; Gaps 1;

QY 69 MKFCQAFKGVNPNIDLESTLYESSVVPKPKAPMDSLFYGYRRHSSDNKRKKII 128  
DB 1 MKFCQAFKGVNPNIDLESTLYESSVVPKPKAPMDSLFYGYRRHSSDNKRKKII 60  
QY 129 EKQSPKAPAPQPPILKVFNRPIFDIVSRGSTADLDGLPELLTHKKRLTDEEPREP 188  
DB 61 EKQSPKAPAPQPPILKVFNRPIFDIVSRGSTADLDGLPELLTHKKRLTDEEPREP 120  
QY 189 STGKTCLPKALLNLSNGRNDIPVLLDIAERTGNMREFINSPFRDIYRGOTALHAIER 248  
DB 121 STGKTCLPKALLNLSNGRNDIPVLLDIAERTGNMREFINSPFRDIYRGOTALHAIER 180  
QY 249 RCKHYVELLVAQADVHAQARGRFQPKDEGGYFYFGLPLSLAECTNQHIVNYLTENP 308  
DB 181 RCKHYVELLVAQADVHAQARGRFQPKDEGGYFYFGLPLSLAECTNQHIVNYLTENP 240  
QY 309 HKKADMRDSDSGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLPDSNLEAVLNN 368  
DB 241 HKKADMRDSDSGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLPDSNLEAVLNN 300  
QY 369 DGLSPLMAAATGIGIFQHIIRREVTDEDRHLSRKFQWAYGPVYSSLYDLSLDTGC 428  
DB 301 DGLSPLMAAATGIGI----- 316

QY 429 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLT 488  
DB 317 -----NRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLCAMVIFTLT 360  
QY 489 AYOPLGTPPYRTVDYLRAGEVITLTGVLFFFTNKKDLFMKPCGVNSLFTDGS 548  
DB 361 AYOPLGTPPYRTVDYLRAGEVITLTGVLFFFTNKKDLFMKPCGVNSLFTDGS 420  
QY 549 FOLLYFIYSLVISAALYLAGIEAYLAVMVYFALVGLGMNLYFTRGLKLTGYSIMIQK 608  
DB 421 FOLLYFIYSLVISAALYLAGIEAYLAVMVYFALVGLGMNLYFTRGLKLTGYSIMIQK 480  
QY 609 ILFKDLFRLLVLLFMIGYASALVSLNPNCAKMKVCNEDQNTCTVTPYPSCRDSEFST 668  
DB 481 ILFKDLFRLLVLLFMIGYASALVSLNPNCAKMKVCNEDQNTCTVTPYPSCRDSEFST 540  
QY 669 FLDDLFLKLTIGMDLEMLSSKYPVVFILVYIILTFVLLNMLIALMGSTVGQVSKE 728  
DB 541 FLDDLFLKLTIGMDLEMLSSKYPVVFILVYIILTFVLLNMLIALMGSTVGQVSKE 600  
QY 729 SKHIWKLOWATTILDIERSPVFLKAFRSGEMVTVGKSDGTPDRRCFRVDEVNWSHW 788  
DB 601 SKHIWKLOWATTILDIERSPVFLKAFRSGEMVTVGKSDGTPDRRCFRVDEVNWSHW 660  
QY 789 NONLGIINEDPGKNETYYGFSHTVGRRLDRWSSVPRVVELNKNPNDEVVVPLDSM 848  
DB 661 NONLGIINEDPGKNETYYGFSHTVGRRLDRWSSVPRVVELNKNPNDEVVVPLDSM 720  
QY 849 GNPRCDGHQOQYPRKWRDDAP 870  
DB 721 GNPRCDGHQOQYPRKWRDDAP 742

RESULT 14

AAE06683  
ID AAE06683 standard; Protein: 742 AA.

XX AC AAE06683;  
XX DT 16-OCT-2001 (first entry)  
XX DE Human vanilloid receptor VR3 isoform, VR3A+B+.  
XX KW Human; vanilloid receptor; VR3; inflammatory condition; analgesic;  
KW intractable pain; postherpetic neuralgia; diabetic neuropathy; asthma;  
KW postmastectomy pain; complex regional pain syndrome; arthritis;  
KW rheumatoid arthritis; osteoarthritis; ulcer; neurodegenerative disease;  
KW chronic obstructive pulmonary disease; irritable bowel syndrome;  
KW psoriasis; central nervous system disease; CNS; cancer;  
KW intestinal tract disorder; VR3A+B+.  
XX OS Homo sapiens.  
XX XX W0200158945-A1.  
XX PN 16-AUG-2001.  
XX PD 01-FEB-2001; 2001WO-US03456.  
XX PF 08-FEB-2000; 2000US-0500123.  
XX PR (ORTH ) ORTHO-MCNEIL PHARM INC.  
XX PA Dublin AE, Huar A, Glass CA, Erlander MG;  
XX PI WPI; 2001-488969/53.  
XX XX N-PSDB; AAD12793.  
XX DR New human VR3 receptor useful for the treatment of disorders including  
XX PT cancers arthritis and pain -  
XX PS Claim 11; Fig 8; 104pp; English.  
XX CC The patent relates to human vanilloid receptor VR3 polynucleotide and  
CC polypeptide. Three isoforms of VR3 namely VR3A+B-, VR3A-B- and VR3A+B+  
CC have also been disclosed. The VR3 polypeptide is used to identify its  
CC modulators which are useful for the treatment of inflammatory conditions  
CC and for use as analgesics for intractable pain associated with  
CC postherpetic neuralgia, diabetic neuropathy, postmastectomy pain, complex  
CC regional pain syndromes, arthritis (e.g. rheumatoid and osteoarthritis),  
CC as well as ulcers, neurodegenerative diseases, asthma, chronic  
CC obstructive pulmonary disease, irritable bowel syndrome and psoriasis.  
CC The VR3 modulators are also useful for treatment of central nervous  
CC system (CNS) diseases, diseases of the intestinal tract, abnormal  
CC proliferation and cancer. The present sequence is human VR3 receptor  
CC isoform, VR3A+B+.  
XX SQ Sequence 742 AA;  
Query Match 83.7%; Score 3829; DB 22; Length 742;  
Best Local Similarity 100.0%; Pred. NO. 0;  
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MADSSGPRAGPGGEVAELPGDESGTGGGEAFPLSSLANLFEDEGSLSPSPADSRPAGP 60  
DB 1 MADSSGPRAGPGGEVAELPGDESGTGGGEAFPLSSLANLFEDEGSLSPSPADSRPAGP 60  
QY 61 GDGRPNLRMKFQGAFRKGVNPNIDLLSTLYESSVVPKPKAPMDSLFDTYGRHSSDN 120  
DB 61 GDGRPNLRMKFQGAFRKGVNPNIDLLSTLYESSVVPKPKAPMDSLFDTYGRHSSDN 120  
QY 121 KRWKKTIEKQPSKAPAPQPPPIKVFNRPIFDIVSRGSTADLDGLLPFLTHKKRL 180  
DB 121 KRWKKTIEKQPSKAPAPQPPPIKVFNRPIFDIVSRGSTADLDGLLPFLTHKKRL 180  
QY 181 TDEEFREPSGTGKCLPKALLNLNSGRNDTIPVLLDIAERTGNMRETFNSFRDIYRGQT 240  
DB 181 TDEEFREPSGTGKCLPKALLNLNSGRNDTIPVLLDIAERTGNMRETFNSFRDIYRGQT 240

QY 241 ALHIAIERRCKHYVELLVAGADVHAQARGFFQPKDEGGYFVGELPLSLAACNPHI 300  
DB 241 ALHIAIERRCKHYVELLVAGADVHAQARGFFQPKDEGGYFVGELPLSLAACNPHI 300  
QY 301 VNYLTENPHKADMRRODSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLEPDS 360  
DB 301 VNYLTENPHKADMRRODSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLEPDS 360  
QY 361 NLEAVLNDGLSPLMMAAKTKIGIFOHIIIRREVTDETRHLSRKFCDWAYGVPYSSLYD 420  
DB 361 NLEAVLNDGLSPLMMAAKTKIGIFOHIIIRREVTDETRHLSRKFCDWAYGVPYSSLYD 420  
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFCGAVSFYINVSYLEC 480  
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFCGAVSFYINVSYLEC 480  
QY 481 AMVIFTLTAYQPLEGTPPYRTTYDYLRLAGEVITLFTGVLFFFTNIDKLMKKCPGV 540  
DB 481 AMVIFTLTAYQPLEGTPPYRTTYDYLRLAGEVITLFTGVLFFFTNIDKLMKKCPGV 540  
QY 541 NSLFIDGSFOLLYFIYSVLVSAALYLAGIETAYLVAMVAFALVGMNALLYFTRGKLTG 600  
DB 541 NSLFIDGSFOLLYFIYSVLVSAALYLAGIETAYLVAMVAFALVGMNALLYFTRGKLTG 600  
QY 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPNCANMKVCNEDQNTCTVPTPSC 660  
DB 601 TYSIMIQKILFKDLFRFLVYLLFMIGYASALVSLNPNCANMKVCNEDQNTCTVPTPSC 660  
QY 661 RDETSFTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720  
DB 661 RDETSFTFLDLFKLTIGMDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720  
QY 721 TVGQVSKESKHIWKLQ 736  
DB 721 TVGQVSKESKHIWKLQ 736  
RESULT 15  
AAU74936  
ID AAU74936 standard; Protein; 602 AA.  
XX AC AAU74936;  
XX DT 23-APR-2002 (first entry)  
XX DE Amino acid sequence of human vanilloid receptor-like protein 2b (VRL-2b).  
XX KW Human; vanilloid receptor-like protein 2b; VRL-2b; hypertension;  
KW ion-channel protein; pain; osteoarthritis; diabetic neuropathy;  
KW neuralgia; nerve injury; neurodegeneration; stroke; inflammation;  
KW asthma; allergy; urogenital disorder; incontinence; hypotension;  
KW perivascular disease; VRL-related disease; receptor.  
XX OS Homo sapiens.  
XX XX EP1160254-A1.  
XX PN 05-DEC-2001.  
XX PD 25-MAY-2001; 2001EP-0304663.  
XX PF 31-MAY-2000; 2000US-208156P.  
XX PR (PFIZ ) PFIZER INC.  
XX PA Shinjo K, Yabuuchi H;  
XX PI WPI; 2002-084359/12.  
XX DR N-PSDB; ABK14003.  
XX DR New human vanilloid receptor-like proteins, useful for identifying  
PT modulators for e.g. treating pain, also related nucleic acid -  
XX

Claim 1; Page 21-22; 32pp; English.

Search completed: June 3, 2003, 19:54:19  
Job time : 76 secs

PS The present invention relates to a new polypeptide that has a sequence  
XX 871 amino acids (AAU74935) or 602 amino acids (AAU74936) long, or their  
CC variants, as defined in the specification. The polypeptide of the  
CC invention is deduced from a human nucleic acid 2749 base pairs (ABK14002)  
CC or 1900 base pairs (ABK14003) long, or their variants, also defined in  
CC the specification. The polypeptides of the invention, which are human  
CC vanilloid receptor-like (VRL) proteins, are used to identify specific  
CC modulators that are potentially useful for treating pain (of any origin),  
CC osteoarthritis, (diabetic) neuropathy, neuralgia, nerve injury,  
CC neurodegeneration, stroke, inflammation, asthma, allergy, urogenital  
CC disorders, incontinence, hypo- or hyper-tension and perivascular disease.  
CC The molecules of the invention can also be used to raise specific  
CC antibodies. The nucleic acid that encodes the polypeptide of the  
CC invention is useful for recombinant production of the protein and for  
CC preparing transgenic animal models. The polypeptide, antibody and nucleic  
CC acid of the invention are also useful as diagnostic agents for  
CC determining (susceptibility to) VRL-related diseases. The present amino  
CC acid sequence represents the human vanilloid receptor-like protein 2b  
CC (VRL-2b) of the invention.  
XX  
SQ Sequence 602 AA;

Query Match 68.2%; Score 3121.5; DB 23; Length 602;  
Best Local Similarity 92.7%; Pred. No. 3.3e-290;  
Matches 601; Conservative 0; Mismatches 0; Indels 47; Gaps 1;  
QY 223 MREINSFPRDIYRGQTALHAIERCKHYVELLVAAQADVHAQAGRRFFQPKDEGYF 282  
DB 1 MREINSFPRDIYR----- 15  
QY 283 YFGLPLSLAACTNQHPIHVNLTENPHKKADMRQDSRGNTVLHALVAIADNTRNTKVF 342  
DB 16 --GELPLSLAACTNQHPIHVNLTENPHKKADMRQDSRGNTVLHALVAIADNTRNTKVF 73  
QY 343 TKMYDLLLKKCARLPPDSNLEAVLNDGLSPLMAAKTGKIGIFQHIIRREVTDEDTRHL 402  
DB 74 TKMYDLLLKKCARLPPDSNLEAVLNDGLSPLMAAKTGKIGIFQHIIRREVTDEDTRHL 133  
QY 403 SRKFKWAYGPVYSSLDLSDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLROK 462  
DB 134 SRKFKWAYGPVYSSLDLSDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLROK 193  
QY 463 WRKFGAVSYINNVSYLCAMVIFLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGV 522  
DB 194 WRKFGAVSYINNVSYLCAMVIFLTAYQPLEGTPPYRTTVDYLRAGEVITLFTGV 253  
QY 523 LFFETNIKDLFMKCPGVNSLFDGSPQLLYFIYSLVIVYSAALYLAGIAYLAVMYFAL 582  
DB 254 LFFETNIKDLFMKCPGVNSLFDGSPQLLYFIYSLVIVYSAALYLAGIAYLAVMYFAL 313  
QY 583 VLGMNNAlyTRGLKLTGYSIMTKILFKDLFRFLVYLLFMIGYASALVSLNPCANM 642  
DB 314 VLGMNNAlyTRGLKLTGYSIMTKILFKDLFRFLVYLLFMIGYASALVSLNPCANM 373  
QY 643 KVCNEDQTNCTVPTYPSCRSETFTFLDLFKLTICMGDLEMLSSTKYPVVFILLVY 702  
DB 374 KVCNEDQTNCTVPTYPSCRSETFTFLDLFKLTICMGDLEMLSSTKYPVVFILLVY 433  
QY 703 IILTFVLLNNLIALMGETGVQSVKESKHWKLOWATTILDIERSPFVFLKAFRSGEMV 762  
DB 434 IILTFVLLNNLIALMGETGVQSVKESKHWKLOWATTILDIERSPFVFLKAFRSGEMV 493  
QY 763 TVGKSSDGTDDRRCFRVDEVNWSHWNQNLGIINEDPGKNETYQYGFSGHTVGLRLDRW 822  
DB 494 TVGKSSDGTDDRRCFRVDEVNWSHWNQNLGIINEDPGKNETYQYGFSGHTVGLRLDRW 553  
QY 823 SSVYPRVVELNKNNDPEVVVPLDSMGNPRCDGHQOQYPRKWRRTDDAP 870  
DB 554 SSVYPRVVELNKNNDPEVVVPLDSMGNPRCDGHQOQYPRKWRRTDDAP 601



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OY 361 NLEAVLNNDGSLPLMAAATGKIGIFQHIIRREVTDTRHLSRKFCKDWAYGCVYSSLYD 420
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Db 361 NLEAVLNNDGSLPLMAAATGKIGIFQHIIRREVTDTRHLSRKFCKDWAYGCVYSSLYD 420
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OY 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLE 480
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Db 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLE 480
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OY 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFPTNIKDLFMKKCPGV 540
|||||
Db 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFPTNIKDLFMKKCPGV 540
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OY 541 NSLFDGSGFQLLYFYISVLYVSAALYLAGIEAYLAVMVFALVGLGMNALYFTRGLKLTG 600
|||||
Db 541 NSLFDGSGFQLLYFYISVLYVSAALYLAGIEAYLAVMVFALVGLGMNALYFTRGLKLTG 600
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OY 601 TYSIMIQILFKDLFRLLVLLFMIGYASALVSLNPCANMKVCNEDQTNCTVPTPSC 660
|||||
Db 601 TYSIMIQILFKDLFRLLVLLFMIGYASALVSLNPCANMKVCNEDQTNCTVPTPSC 660
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OY 661 RDSFTFSLDLFLKLTIGMDLEMLSTKYPVVFIILLVYIILTFVLLNMLIALMGE 720
|||||
Db 661 RDSFTFSLDLFLKLTIGMDLEMLSTKYPVVFIILLVYIILTFVLLNMLIALMGE 720
|||||
OY 721 TVGQVSKESKHINKLOWATTIILDIERSPPVFLRKAFRSGEMVTYCKSSDGTDDRWCFRV 780
|||||
Db 721 TVGQVSKESKHINKLOWATTIILDIERSPPVFLRKAFRSGEMVTYCKSSDGTDDRWCFRV 780
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OY 781 DEVNWSHWNQNLGIINEDPGKNETYYQYGFSTVGRLLRRDRWSSVPRVVELNKNNSPDE 840
|||||
Db 781 DEVNWSHWNQNLGIINEDPGKNETYYQYGFSTVGRLLRRDRWSSVPRVVELNKNNSPDE 840
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OY 841 VVPLDSMGNPCDGHQGYPRKWRRTDAP 870
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Db 841 VVPLDSMGNPCDGHQGYPRKWRRTDAP 870
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```

## RESULT 2

```
US-09-500-123-9
; Sequence 9, Application US/09500123
; Patent No. 6455278
; GENERAL INFORMATION:
; APPLICANT: Dublin, Adrienne E
; APPLICANT: Huvar, Arne
; APPLICANT: Erlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
; FILE REFERENCE: Human VR3
; CURRENT APPLICATION NUMBER: US/09/500,123
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 811
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-500-123-9
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Query Match 92.2%; Score 4218; DB 4; Length 811.
Best Local Similarity 93.0%; Pred. No. 0;
Matches 809; Conservative 0; Mismatches 1; Indels 60; Gaps 1;

OY 1 MADSSGPRAGGVAELPGDESGTGGGEAFPLSSLANLFEDEGSLSPSPADASRAGP 60
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Db 1 MADSSGPRAGGVAELPGDESGTGGGEAFPLSSLANLFEDEGSLSPSPADASRAGP 60
|||||
OY 61 GDGRPNLRMKFQGAFRKGVNPDILLSTLYESSVWPGPKAPMDSLFDYGYTRHSSDN 120
|||||
Db 61 GDGRPNLRMKFQGAFRKGVNPDILLSTLYESSVWPGPKAPMDSLFDYGYTRHSSDN 120
|||||
OY 121 KWRKKKIIKOPQSPKAPAPQPPILKVFNRPIILFDIVSRGSTADLGLLFFLLTHKKRL 180
|||||
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```
Db 121 KWRKKKIIKOPQSPKAPAPQPPILKVFNRPIILFDIVSRGSTADLGLLFFLLTHKKRL 180
|||||
OY 181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPLVLDIAERTGNMREFINSPPRDIYRGQT 240
|||||
Db 181 TDEEFREPSTGKTCLPKALLNLSNGRNDTIPLVLDIAERTGNMREFINSPPRDIYRGQT 240
|||||
OY 241 ALHTAIERRCHYVELLYVAQADYHAQARGFFQPKDEGGYFYFGELPLSLAECTNQPHI 300
|||||
Db 241 ALHTAIERRCHYVELLYVAQADYHAQARGFFQPKDEGGYFYFGELPLSLAECTNQPHI 300
|||||
OY 301 VNYLTENPHKKADRRRODSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLFPDS 360
|||||
Db 301 VNYLTENPHKKADRRRODSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLFPDS 360
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OY 361 NLEAVLNNDGSLPLMAAATKOKIGIFQHIIRREVTDTRHLSRKFCKDWAYGCVYSSLYD 420
|||||
Db 361 NLEAVLNNDGSLPLMAAATG----- 381
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OY 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLE 480
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Db 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLE 480
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OY 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFPTNIKDLFMKKCPGV 540
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Db 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFPTNIKDLFMKKCPGV 540
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OY 541 NSLFDGSGFQLLYFYISVLYVSAALYLAGIEAYLAVMVFALVGLGMNALYFTRGLKLTG 600
|||||
Db 541 NSLFDGSGFQLLYFYISVLYVSAALYLAGIEAYLAVMVFALVGLGMNALYFTRGLKLTG 600
|||||
OY 601 TYSIMIQILFKDLFRLLVLLFMIGYASALVSLNPCANMKVCNEDQTNCTVPTPSC 660
|||||
Db 601 TYSIMIQILFKDLFRLLVLLFMIGYASALVSLNPCANMKVCNEDQTNCTVPTPSC 660
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OY 661 RDSFTFSLDLFLKLTIGMDLEMLSTKYPVVFIILLVYIILTFVLLNMLIALMGE 720
|||||
Db 661 RDSFTFSLDLFLKLTIGMDLEMLSTKYPVVFIILLVYIILTFVLLNMLIALMGE 720
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OY 721 TVGQVSKESKHINKLOWATTIILDIERSPPVFLRKAFRSGEMVTYCKSSDGTDDRWCFRV 780
|||||
Db 721 TVGQVSKESKHINKLOWATTIILDIERSPPVFLRKAFRSGEMVTYCKSSDGTDDRWCFRV 780
|||||
OY 781 DEVNWSHWNQNLGIINEDPGKNETYYQYGFSTVGRLLRRDRWSSVPRVVELNKNNSPDE 840
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Db 781 DEVNWSHWNQNLGIINEDPGKNETYYQYGFSTVGRLLRRDRWSSVPRVVELNKNNSPDE 840
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OY 841 VVPLDSMGNPCDGHQGYPRKWRRTDAP 870
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Db 841 VVPLDSMGNPCDGHQGYPRKWRRTDAP 870
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## RESULT 3

```
US-09-500-123-12
; Sequence 12, Application US/09500123
; Patent No. 6455278
; GENERAL INFORMATION:
; APPLICANT: Dublin, Adrienne E
; APPLICANT: Huvar, Arne
; APPLICANT: Erlander, Mark G
; APPLICANT: Glass, Charles A
; TITLE OF INVENTION: DNA encoding Isoforms of the human Vanilloid Receptor
; FILE REFERENCE: Human VR3
; CURRENT APPLICATION NUMBER: US/09/500,123
; CURRENT FILING DATE: 2000-02-08
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-500-123-12
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Query Match 83.7%; Score 3829; DB 4; Length 742;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 736; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADSSGPRAGPCEVAELPGDESGTGGGAFFPLSSLANLFEDEGDSGLSPSPADASRPGP 60  
DB 1 MADSSGPRAGPCEVAELPGDESGTGGGAFFPLSSLANLFEDEGDSGLSPSPADASRPGP 60

QY 61 GDGRPNLRMKFOGAFRKGVPNPIDLLLESTLYESSVVPKPKAPMDSLFDFYGTYYRHSSDN 120  
DB 61 GDGRPNLRMKFOGAFRKGVPNPIDLLLESTLYESSVVPKPKAPMDSLFDFYGTYYRHSSDN 120

QY 121 KWRKKIIEKQSPKAPAPQPPPIKLVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180  
DB 121 KWRKKIIEKQSPKAPAPQPPPIKLVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180

QY 181 TDEEFREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNRMREINSPFRDIYRGOT 240  
DB 181 TDEEFREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNRMREINSPFRDIYRGOT 240

QY 241 ALHIAIERCKKHVVELLVQAQADVHAQARFPQKDEGGYFYFGEPLPLSLAACTNPHI 300  
DB 241 ALHIAIERCKKHVVELLVQAQADVHAQARFPQKDEGGYFYFGEPLPLSLAACTNPHI 300

QY 301 VNYLTENPHKKADMRQDSRGNTVHALVAIAADNTRENTKFTVMYDLLLLKCARLPDS 360  
DB 301 VNYLTENPHKKADMRQDSRGNTVHALVAIAADNTRENTKFTVMYDLLLLKCARLPDS 360

QY 361 NLEAVLNNDGLSPLMAAATGKIGIFQHIIRREVTDETRHLSRKFEDWAYGVPYSSLYD 420  
DB 361 NLEAVLNNDGLSPLMAAATGKIGIFQHIIRREVTDETRHLSRKFEDWAYGVPYSSLYD 420

QY 421 LSSLDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFCGAVSFYINVSYLEC 480  
DB 421 LSSLDTCGGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFCGAVSFYINVSYLEC 480

QY 481 AMVIFLTAYOPLCTPPYPTVTDYLRRLAGEVITLFTGVLFNFKDLMFKKCPGV 540  
DB 481 AMVIFLTAYOPLCTPPYPTVTDYLRRLAGEVITLFTGVLFNFKDLMFKKCPGV 540

QY 541 NSLFDIGSQLLLYFYISLVIVSAALYLAGIEAYLAVMVFALVGLWMNALYFTRGLKLTG 600  
DB 541 NSLFDIGSQLLLYFYISLVIVSAALYLAGIEAYLAVMVFALVGLWMNALYFTRGLKLTG 600

QY 601 TYSIMTOKILFKDLRFLAVLLEFMIGYASALVSLNLANPCANMKVCNEDOTNCTVTPSC 660  
DB 601 TYSIMTOKILFKDLRFLAVLLEFMIGYASALVSLNLANPCANMKVCNEDOTNCTVTPSC 660

QY 661 RDSFTSTFLDLFKLTIGMDLEMLSSSTKYPVVFILLVYIILTFVLLNMLIALMGE 720  
DB 661 RDSFTSTFLDLFKLTIGMDLEMLSSSTKYPVVFILLVYIILTFVLLNMLIALMGE 720

QY 721 TVGQVSKESKHWWKLQ 736  
DB 721 TVGQVSKESKHWWKLQ 736

RESULT 4  
US-09-235-451-25  
; Sequence 25, Application US/09235451  
; GENERAL INFORMATION:  
; APPLICANT: Julius, David J.  
; APPLICANT: Caterina, Michael J.  
; APPLICANT: Brake, Anthony J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING  
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED  
; FILE OF INVENTION: POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: 9076/084CIP  
; CURRENT APPLICATION NUMBER: US/09/235,451  
; CURRENT FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/072,151  
; PRIOR FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: 08/915,461

; PRIOR FILING DATE: 1997-08-20  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 25  
; LENGTH: 843  
; TYPE: PRT  
; ORGANISM: chicken  
US-09-235-451-25

Query Match 40.3%; Score 1845.5; DB 4; Length 843;  
Best Local Similarity 46.3%; Pred. No. 1.6e-163;  
Matches 399; Conservative 150; Mismatches 227; Indels 85; Gaps 23;

QY 41 EGEDGSLSPADASRPGPGGRPNLRMKFOGAFRKGVPNPIDLLLESTLY--ESSVVP 98  
DB 27 DGEDSAL--ETAD-----NLOGT-----SNKVQPSKSNIFARRGRFV 64

QY 99 ---PKAPMDSLFY-----GTYRHSSDNKWRKKIIEKQ---OSPKAPQPPIL 146  
DB 65 DCDKMAPMDSFYQMDHLMAPSVIKPHANMERGKLHLLSTDSITGCSKA-----F 116

QY 147 KVENRPILFDIVSRGSTADLDGLLPFLTHKKRLTDEEFREPSTGKTCPLKALLNSGR 206  
DB 117 KFYDRRIIFDAVARGSTKDLDDLLLYLNRTHLTDDEFPKPEGTGTCCLKAWLNHDGK 176

QY 207 NDTIPVLLDIAERTGNRMREINSPFRDIYRGOTALHIAIERCKKHVVELLVQAQADVHA 266  
DB 177 NDTIPVLLDIAERTGTLKEFVNAEYTDNYKGTALHIAIERNMVYLKLLVONGADVHA 236

QY 267 QARGRFQP-KDEGGYFYFGEPLPLSLAACTNPHIYNTENPHKKADMRQDSRGNTVL 325  
DB 237 RACGEFPRKIKGPG-FYFGEPLPLSLAACTNOLCIVKLEENPYQAADAAEDSMGMVL 295

QY 326 HALVAIADNTRENTKFTVMYDLLLLKCARLPDSNLEAVLNNDGLSPLMAAATGKIGI 385  
DB 296 HLTVEIADNTKONTKFTVMYNNILGAKINPILKLEBLTNKKGLTTLTAAKTGKIGI 355

QY 386 FOHITRREYTDTRHLSRKFEDWAYGVPYSSLYDLSLDTGCEASVLEILVYNSKIEN 445  
DB 356 FAYILRREIKDPECRLHLSRKFTEWAYGVPVHSSLYDLSLDTGCEASVLEILVYNSKIEN 414

QY 446 RHEMLAVEPINELLRDKWRKFCGAVSFYINVSYLCAWITFTTAYVQPLE--GTPPY 502  
DB 415 RHEMLAVEPINELLRDKWRKFCGAVSFYINVSYLCAWITFTTAYVQPLE--GTPPY 474

QY 503 RTVDYLRRLAGEVITLFTGVLFNFKDLMFKKCPGVNSLFDIGSQLLLYFYISLVIV 562  
DB 475 HSTGEYFRTVGTILSVGLGLYFFFRGIQ-YFVQRRESLKTLIVDSYSEVLFVHSL 533

QY 563 SAALYLAGIEAYLAVMVFALVGLWMNALYFTRGLKLTGTYSIMIQILFKDLRFLAVL 622  
DB 534 SVLVFCGQELVAVSMVFSALGANMLYTRGFOQMGYISVYIAKMLIRDLRCRFVYL 593

QY 623 LFMIGYASALVSLNLANPCANMKVCNEDO-TNCTVTPYPCORDETST-----FLDL 674  
DB 594 VFLGFTSTAVTLLIED-----DNEGQDTNSS--EYARCSHTKRGTSYNSLYTCTELF 645

QY 675 KLTIGMDLEMLSSSTKYPVVFILLVYIILTFVLLNMLIALMGETVQVSKESKHWW 734  
DB 646 KFTIGMDLEFTENYRFSKVSFVILVYLVYIILTFVLLNMLIALMGETVQVSKESKHWW 705

QY 735 LQWATTILDIERSFVFLKAFRSGEMVTGKSSDGTDPDRRCFCFVDEYVNSHWNONLGI 794  
DB 706 LQRPITILDIENSYNCLRSRSGKRVLGITPDGDDYRWCFCFVDEYVNSHWNONLGI 765

QY 795 INEDPG-----KNETYQYGFSTVGRRLRRDWSVPRVVELKNSN----PDEVV 844  
DB 766 INEDPGSGDLKRNPSY-----CIKPRVSGKNKTLVPLLRDGSRRTEPKLPEIKL 820

QY 845 --LDSMGNPR-CDGHQOQYPR 862  
DB 821 PILEPYEPEDCETLKESLPK 841

```
RESULT 5
US-09-235-451-2
: Sequence 2, Application US/09233451
: GENERAL INFORMATION:
: APPLICANT: Julius David J.
: APPLICANT: Caterina, Michael J.
: APPLICANT: Brake, Anthony J.
: TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING
: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED
: POLYPEPTIDES AND USES THEREOF
: TITLE OF INVENTION: 9076/084CIP
: CURRENT APPLICATION NUMBER: US/09/235,451
: CURRENT FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/072,151
: PRIOR FILING DATE: 1998-01-22
: PRIOR APPLICATION NUMBER: 08/915,461
: PRIOR FILING DATE: 1997-08-20
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 838
: TYPE: PRT
: ORGANISM: R. rattus
US-09-235-451-2

Query Match          39.7%; Score 1818; DB 4; Length 838;
Best Local Similarity 45.6%; Pred. No. 6e-161;
Matches 388; Conservative 141; Mismatches 222; Indels 100; Gaps 18;

Qy 16 AELPGDESGTPGGE-----APLSSLANLFEDEGSLSPSPADA 54
Db 5 ASLSESESPPOENSCLDPPDRPNCKPPVPKPHFTTSTRTRLF-GKGDSEASPLDC 63
Qy 55 SRPAGCGDGRPNRMKFOGAFRGVNP-PIDLESTLYESSVVPKPKAPMDSLFDYGT 113
Db 64 PYEG-----GLASCIITVSSVL-----TIQPCDGP-----ASV 94
Qy 114 RHSSDNKRWRKIIKQKQSPKAPAPQPPPIKLVFNRPILFDIVSRGSTADLDGLL 173
Db 95 RPSSQDS-----VSAGEKPP--RLYDRRSIFDAVAQSNCOELESLLPFL 136
Qy 174 LTHKKRLTDEEFREPSTGKTCPLKALLNLSNGRNDIPVLLDIAERTGNMREINSPFRD 233
Db 137 QRKKRLTUSEFKDPETGKTCLLKAMLNHNGONDIALLDVARKTDSLKQFVNASYTD 196
Qy 234 IYRGOTALHIAIERCKHYVELLVAGQADVHAQAARGFPQKDEGGYFYFGEPLSLAA 293
Db 197 SYVGOTALHIAIERNNMTLVTLVENGADVQAANGDFKTKGRPGFYFGEPLSLAA 256
Qy 294 CTNPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKC 353
Db 257 CTNQLATVKFLLQNSQPADISARDSVGNLHALVEADNTVDNTKFTVMYNEILIG 316
Qy 354 ARLPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIIRREVTDEDTRHLSRKFKNAYGP 413
Db 317 AKLHPTLKEETNRKGLTPLAASGKIGVLAYILQREIHEPECHLSRKFKNAYGP 376
Qy 414 VYSLDLSLDCGGEASVLEILVY-NSKIENRHEMLAVEPTNELLRDKWRKFGAVSFY 472
Db 377 VHSLLDLCIDTC-EKNSVLEIAYISSSETPNRHMVLLPELNRLLQDKWDRFVRIFY 435
Qy 473 INVYSYLCAMVIFTLAYOPLGTPPYRTTV-DYLRAGEVITLFTGVLFFTNID 531
Db 436 FNEFVYCLYMIIFTAAAYRPVPSGLPPYKLNVTGDFRVYTGILSVSGVYFFRGIO- 494
Qy 532 LFMKKCPGNSLFDIGSFOLLFIYSVLVIVSAALYAGIEAYLVAVWVFLVGNWALY 591
Db 495 YFQRRPSLKSFLVDSYSEILFFVQSLFVLVSVLYFSQRKEYVASNVFSLAMGWNMLY 554
Qy 592 FTRGLKLTGYSTMICKILFKDLFRLLVTLFPMICYASALVSLLANPCANMKVCNEDQTN 651
Db 555 YTRGFOQMGIYAVMIKMIILRDLRFMFVTLFVLFGLFSTAVVTLI-----EDGKN 604

US-09-132-316-3
: Sequence 3, Application US/091323168
: Patent No. 644440
: GENERAL INFORMATION:
: APPLICANT: Young, Paul E.
: APPLICANT: Ruben, Steven M.
: TITLE OF INVENTION: Vanilloid Receptor-2
: FILE REFERENCE: 1488.1110000
: CURRENT APPLICATION NUMBER: US/09/132,316B
: CURRENT FILING DATE: 1998-08-11
: EARLIER APPLICATION NUMBER: US 60/040,163
: EARLIER FILING DATE: 1997-03-07
: EARLIER APPLICATION NUMBER: PCT/US98/04493
: EARLIER FILING DATE: 1998-03-06
: NUMBER OF SEQ ID NOS: 67
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 3
: LENGTH: 838
: TYPE: PRT
: ORGANISM: Rattus norvegicus
US-09-132-316-3

Query Match          39.7%; Score 1818; DB 4; Length 838;
Best Local Similarity 45.8%; Pred. No. 6e-161;
Matches 388; Conservative 141; Mismatches 222; Indels 100; Gaps 18;

Qy 16 AELPGDESGTPGGE-----APLSSLANLFEDEGSLSPSPADA 54
Db 5 ASLSESESPPOENSCLDPPDRPNCKPPVPKPHFTTSTRTRLF-GKGDSEASPLDC 63
Qy 55 SRPAGCGDGRPNRMKFOGAFRGVNP-PIDLESTLYESSVVPKPKAPMDSLFDYGT 113
Db 64 PYEG-----GLASCIITVSSVL-----TIQPCDGP-----ASV 94
Qy 114 RHSSDNKRWRKIIKQKQSPKAPAPQPPPIKLVFNRPILFDIVSRGSTADLDGLL 173
Db 95 RPSSQDS-----VSAGEKPP--RLYDRRSIFDAVAQSNCOELESLLPFL 136
Qy 174 LTHKKRLTDEEFREPSTGKTCPLKALLNLSNGRNDIPVLLDIAERTGNMREINSPFRD 233
Db 137 QRKKRLTUSEFKDPETGKTCLLKAMLNHNGONDIALLDVARKTDSLKQFVNASYTD 196
Qy 234 IYRGOTALHIAIERCKHYVELLVAGQADVHAQAARGFPQKDEGGYFYFGEPLSLAA 293
Db 197 SYVGOTALHIAIERNNMTLVTLVENGADVQAANGDFKTKGRPGFYFGEPLSLAA 256
Qy 294 CTNPHIVNYLTENPHKKADMRRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKC 353
Db 257 CTNQLATVKFLLQNSQPADISARDSVGNLHALVEADNTVDNTKFTVMYNEILIG 316
Qy 354 ARLPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIIRREVTDEDTRHLSRKFKNAYGP 413
Db 317 AKLHPTLKEETNRKGLTPLAASGKIGVLAYILQREIHEPECHLSRKFKNAYGP 376
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US-09-197-636-8

; Sequence 8, Application US/09197636  
; Patent No. 6239267  
; GENERAL INFORMATION:  
; APPLICANT: DUCKWORTH, DAVID  
; APPLICANT: HAYES, PHILIP  
; APPLICANT: MEADOWS, HELEN  
; APPLICANT: DAVIS, JOHN  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ratner & Prestia  
; STREET: P.O. Box 980  
; CITY: Valley Forge  
; STATE: PA  
; COUNTRY: US  
; ZIP: 19482-0980  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/197,636  
; FILING DATE: 23-NOV-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: UK 9805137.8  
; FILING DATE: 12-MAR-1998  
; APPLICATION NUMBER: UK 9815791.0  
; FILING DATE: 21-JUL-1998  
; APPLICATION NUMBER: UK 9819278.4  
; FILING DATE: 03-SEP-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Prestia, Paul F  
; REGISTRATION NUMBER: 23,031  
; REFERENCE/DOCKET NUMBER: GP-30075  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 601-407-0700  
; TELEFAX: 610-407-0701  
; TELEX: 846169  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 839 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-197-636-8

Query Match 39.3%; Score 1800; DB 4; Length 839;  
Best Local Similarity 44.9%; Pred. No. 2.9e-159;  
Matches 374; Conservative 156; Mismatches 222; Indels 81; Gaps 15;  
QY 49 PSPADASRAGPDCGRPNL-----RMKFG-----AFKGVNPNIDLES--TLYESV 95  
Db 22 PDLPGDPSRRPPAKPOLSTAKSRTLFGKGDSEAFVDCPHEBGELDSCTITVSPV 81  
QY 96 V-----PGPKAPMDSLFYGYTHRHSSDNKRWRKKIIEKQPSPKAPAPPPILKVF 149  
Db 82 ITIQRPGDGTGARL-----LSQDSVAASTEKTLRLY 113  
QY 150 NRPILFDVSRGSTADGLPLFLTHKKRLTDEEFREPSTGKTCPLKALLNSGRNDT 209  
Db 114 DRSIFEVAQNCCODESLFLQSKKHLTDNEFKDPETGKTCCLKAMNLHDQNTT 173  
QY 210 IPVLIDIAERTGNMREFINSFEDYRQGTALHTAIERCKHYVELLVAQADVHAQAR 269  
Db 174 IPLLIEIARQTSKLKELVNASYTSYKGTALHTAIERRNALVTLVENGADVOAAH 233  
QY 270 GRFFQPKDEGGYFYFCFGLPLSLAACTNQPHVNYLTENPHKKADMRRODSRGNTVLHALV 329  
Db 234 GDFFKTKRPGFYFGELPLSLAACTNQLGIKFLNLSQWOTADISARDSVGNVLHALV 293

QY 330 AIADNTRENTKFTVMYDLLLLKCARLFPDSNEAVLNNDGLSPLMMAKTGIGIFOHI 389  
Db 294 EVADNTADNTKFTVMYNEILILGAKLHPTKLEELTNKKGMPPLAALAGTGKIGLAYI 353  
QY 390 IRREVTDDETRHLSRPFKDWAYGPVYSSLYDLSSDTCGEASVLEILYV-NSKIENRHE 448  
Db 354 LOREIOPECHLSRPFKTEWAYGPVHSSLYDLSDIDTC-EKNSVLEVIAYSSSETPNRHD 412  
QY 449 MLAVEPINELLRDKWRKFGAVSYINVSYLCAWIFTLTAYTOPLEGTPPYVYRTVDY 508  
Db 413 MLLVEPLNRLLOKQWDRFYKRIEYFNFLVYCLWIFLTAAYYRPVDGLPPFKMEKTDY 472  
QY 509 LRLAGEVITLFTGVLEFFFTNIKDLFMKKCGVNSLFDIGSFQLLYFIYSVLVIVSAALYL 568  
Db 473 FRYTGEILSVLGVYFFFRGIQ-YFLQRRPSMKTFLFVDSYSEMLFFLQSLFMLATVVLYF 531  
QY 569 AGIEAYLAVMVFALVGLGMNNAFYTRGLKLTGYSTMIQILFKDLFRLLVLLFWIGY 628  
Db 532 SHLKEYVASWVSLALGWTNMLYTRFGQOMGIYAVNIEKMILRDLCRFMVFVYVFLGF 591  
QY 629 ASALVSLNPPCANMKVCNEDOTNCTVPTY-----PSCRDSET-----FSTFLDLDFK 675  
Db 592 STAVTILI-----EDGKNDLSPSESTSHRWGCPACRPPDSSYNSLYST-CLELKF 640  
QY 676 LTIGMGDLEMLSTKYVVFVFIILLVYIILTFVLLNMLIALMGETVGVQSKESHIWKL 735  
Db 641 FTIGMGDLEFTENYDFKAVFIILLAYVILTYILLNMLIALMGETVNVKIAQESKNIKWL 700  
QY 736 QWATTTILDIERSPFVFLKAFRSGEMVTYVKGSDGTPDRRCWCPDRVDEVNSHWNQGLII 795  
Db 701 QRAITILDTEKSLFKCMKRAFRSGKLQVGYTPDGKDDYRWCFRVDEVNMTTNTNVGII 760  
QY 796 NEDPGKNE-TYOYVGFSTVGLRRDRWS--SVVPRVVELN---KNSNPDEV 841  
Db 761 NEDPGNCEGVKRTLSFSLSSRSVGRHWKFNALVPLLRASARDROSAOPEV 813

RESULT 9

US-09-235-451-34  
; Sequence 34, Application US/09235451  
; GENERAL INFORMATION:  
; APPLICANT: Julius, David J.  
; APPLICANT: Caterina, Michael J.  
; APPLICANT: Brake, Anthony J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING  
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED  
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: 9076/084CIP  
; CURRENT APPLICATION NUMBER: US/09/235,451  
; CURRENT FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/072,151  
; PRIOR FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: 08/915,461  
; PRIOR FILING DATE: 1997-08-20  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 34  
; LENGTH: 839  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-235-451-34

Query Match 39.3%; Score 1800; DB 4; Length 839;  
Best Local Similarity 44.9%; Pred. No. 2.9e-159;  
Matches 374; Conservative 156; Mismatches 222; Indels 81; Gaps 15;  
QY 49 PSPADASRAGPDCGRPNL-----RMKFG-----AFKGVNPNIDLES--TLYESV 95  
Db 22 PDLPGDPSRRPPAKPOLSTAKSRTLFGKGDSEAFVDCPHEBGELDSCTITVSPV 81  
QY 96 V-----PGPKAPMDSLFYGYTHRHSSDNKRWRKKIIEKQPSPKAPAPPPILKVF 149

Db 82 ITIQRPGDPTGARL-----LSODSVAASTEKTRLRY 113  
QY 150 NRPILFDIVSRGSTADLGLPFLTHKKRLTDEEFPSTGKTCLPKALLNLSNRNDT 209  
Db 114 DRSIFEVAQNCCODESLLFLQKSKKHLTDNEFKDPETKCTCLLKAMLNLDGQNTT 173  
QY 210 IVDLIDIAERTGNMREFINSPPRDIIYRGOTAHIAIERCKHYVELLVAAQADVHAQAR 269  
Db 174 IPLLIEARQOTDSLKELVNASYDSYKGTOTAHIAIERNNMALVTLLVENGADVQAAAH 233  
QY 270 GRFPQKDEGGYFEGELPPLSLAAGTNGPFIYNYLTENPHKKADMRROSGRNTVHLALV 329  
Db 234 GDFFKTKRPGFYFEGELPPLSLAAGTNGPFIYNYLTENPHKKADMRROSGRNTVHLALV 293  
QY 330 ATADTNTRENTKVTMYDLKLCARLPDSNLEAVLNNDGLSPLMMAAKTKIGIFOHI 389  
Db 294 EVADNTADNTKVTSMYNEILLGAKLHPTLKEELTNKGMPLAALAGTKIGVLA 353  
QY 449 MLAVEPINELLRDKKRGKGVAFYINVSYLCAWIFLTAYIQPLEGTPPYPTTVDY 508  
Db 413 MLLVEPLNRLQDKKDRFVKRIFYFNFLVCLYMIIFTMAAYRVPDGLPPFKMEKTGDY 472  
QY 509 LRLAGEVITLFTGVLFVFFFTNIDKLFMKKCPGVNSLFDGSGFOLLFIYSVLVISAAALV 568  
Db 473 FRVTGEILSVLGGVYFFFRGQI-YFLQRRPSMKTFLFVDSYSEMLFFLOSLFMTATVLF 531  
QY 569 AGIEAYLAVMVFALVGLMGNALYFTRGLKLTGYISIMIKILFKDLFRLLVLLFMIGY 628  
Db 532 SHLKEYVASMFSLAGTWNMLYTRGFQOMGIYAVMIEKMLRDLCRFMFYVVFLLFGF 591  
QY 629 ASALVSLNPNCAKMKVCNEDQNTCTVPTY-----PSCRSET-----FSTFLDLDFK 675  
Db 592 STAVVTLI-----EDKNDLSPSESTSHRWRGPACRPPDSSYSLYST-CLELFK 640  
QY 676 LTIGMDLEMSSTKYPVVFIILVYIILTVLLNMLIALMGETVGVSKESKHIWKL 735  
Db 641 FTIGMDLEFTENYDFKAVFIILLYVILYVILLNMLIALMGETVGVSKESKHIWKL 700  
QY 736 QWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDPDRRCFRVDEYNWHSNQLGII 795  
Db 701 QRAITILDTEKSFCLKMRKAFRSGKLLQVGYTPDGKDDYRWCFRVDENWNTWNTNNGII 760  
QY 796 NEDPKNE-TQYGYGFSHTVGRLLRDRWS--SVWPRVVELN-----KNSNPDEV 841  
Db 761 NEDPNCCEGVKRTLSFSLRSSRVSGRHKMKNFALVPLLRASARDRQSAQPEV 813

RESULT 10  
US-09-533-220A-2  
; Sequence 2, Application US/09533220A  
; Patent No. 6406908  
; GENERAL INFORMATION:  
; APPLICANT: McIntyre, Peter  
; APPLICANT: James, Iain Fraser  
; TITLE OF INVENTION: Human Vanilloid Receptor  
; FILE REFERENCE: 4-30875A  
; CURRENT APPLICATION NUMBER: US/09/533,220A  
; CURRENT FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: UNITED KINGDOM 9507097.1  
; PRIOR FILING DATE: 1999-03-26  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 1.30  
; SEQ ID NO 2  
; LENGTH: 839  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-533-220A-2

Query Match 39.3%; Score 1799; DB 4; Length 839;

Best Local Similarity 44.9%; Pred. No. 3.6e-159;  
Matches 374; Conservative 155; Mismatches 223; Indels 81; Gaps 15;  
QY 49 PSPADASRPPAGCDGRPNL-----RMKFG-----AFKGVNPNIDLLS--TLYESSV 95  
Db 22 DPDLGDPNRSRPPAKPOLSTAKSRTRLFCKGDSSEAFVDCPHEGEGLDSCPTIVPSV 81  
QY 96 V-----PGPKAPMDSLFYGTYRHHSSDNKRWRKIIKEQOPSPKAPAPQPPTLVKF 149  
Db 82 ITIQRPGDPTGARL-----LSODSVAASTEKTRLRY 113  
QY 150 NRPILFDIVSRGSTADLGLPFLTHKKRLTDEEFPSTGKTCLPKALLNLSNRNDT 209  
Db 114 DRSIFEVAQNCCODESLLFLQKSKKHLTDNEFKDPETKCTCLLKAMLNLDGQNTT 173  
QY 210 IVDLIDIAERTGNMREFINSPPRDIIYRGOTAHIAIERCKHYVELLVAAQADVHAQAR 269  
Db 174 IPLLIEARQOTDSLKELVNASYDSYKGTOTAHIAIERNNMALVTLLVENGADVQAAAH 233  
QY 270 GRFPQKDEGGYFEGELPPLSLAAGTNGPFIYNYLTENPHKKADMRROSGRNTVHLALV 329  
Db 234 GDFFKTKRPGFYFEGELPPLSLAAGTNGPFIYNYLTENPHKKADMRROSGRNTVHLALV 293  
QY 330 ATADTNTRENTKVTMYDLKLCARLPDSNLEAVLNNDGLSPLMMAAKTKIGIFOHI 389  
Db 294 EVADNTADNTKVTSMYNEILLGAKLHPTLKEELTNKGMPLAALAGTKIGVLA 353  
QY 390 IREVTDETRHLSRKFKDWAYGPVSSYLSLSDTDCGEASVLEILVY-NSKTENRHE 448  
Db 354 LQREIQEPECHLSRKFKTEWAYGPVHSSLYLSDCITC-EKNSVLEVIAYSSSETPNRHD 412  
QY 449 MLAVEPINELLRDKKRGKGVAFYINVSYLCAWIFLTAYIQPLEGTPPYPTTVDY 508  
Db 413 MLLVEPLNRLQDKKDRFVKRIFYFNFLVCLYMIIFTMAAYRVPDGLPPFKMEKTGDY 472  
QY 509 LRLAGEVITLFTGVLFVFFFTNIDKLFMKKCPGVNSLFDGSGFOLLFIYSVLVISAAALV 568  
Db 473 FRVTGEILSVLGGVYFFFRGQI-YFLQRRPSMKTFLFVDSYSEMLFFLOSLFMTATVLF 531  
QY 569 AGIEAYLAVMVFALVGLMGNALYFTRGLKLTGYISIMIKILFKDLFRLLVLLFMIGY 628  
Db 532 SHLKEYVASMFSLAGTWNMLYTRGFQOMGIYAVMIEKMLRDLCRFMFYVVFLLFGF 591  
QY 629 ASALVSLNPNCAKMKVCNEDQNTCTVPTY-----PSCRSET-----FSTFLDLDFK 675  
Db 592 STAVVTLI-----EDKNDLSPSESTSHRWRGPACRPPDSSYSLYST-CLELFK 640  
QY 676 LTIGMDLEMSSTKYPVVFIILVYIILTVLLNMLIALMGETVGVSKESKHIWKL 735  
Db 641 FTIGMDLEFTENYDFKAVFIILLYVILYVILLNMLIALMGETVGVSKESKHIWKL 700  
QY 736 QWATTILDIERSFPVFLKAFRSGEMVTGKSSDGTDPDRRCFRVDEYNWHSNQLGII 795  
Db 701 QRAITILDTEKSFCLKMRKAFRSGKLLQVGYTPDGKDDYRWCFRVDENWNTWNTNNGII 760  
QY 796 NEDPKNE-TQYGYGFSHTVGRLLRDRWS--SVWPRVVELN-----KNSNPDEV 841  
Db 761 NEDPNCCEGVKRTLSFSLRSSRVSGRHKMKNFALVPLLRASARDRQSAQPEV 813

RESULT 11  
US-09-197-636-4  
; Sequence 4, Application US/09197636  
; Patent No. 6239267  
; GENERAL INFORMATION:  
; APPLICANT: DUCKWORTH, DAVID  
; APPLICANT: HAYES, PHILIP  
; APPLICANT: MEADOWS, HELEN  
; APPLICANT: DAVIS, JOHN  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ratner & Prestia

STREET: P.O. Box 980  
 CITY: Valley Forge  
 STATE: PA  
 COUNTRY: US  
 ZIP: 19482-0980  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/197,636  
 FILING DATE: 23-NOV-1998  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: UK 9805137.8  
 FILING DATE: 12-MAR-1998  
 APPLICATION NUMBER: UK 9815791.0  
 FILING DATE: 21-JUL-1998  
 APPLICATION NUMBER: UK 9819278.4  
 FILING DATE: 03-SEP-1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Prestlia, Paul F  
 REGISTRATION NUMBER: 23,031  
 REFERENCE/DOCKET NUMBER: GP-30075  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 601-407-0700  
 TELEFAX: 610-407-0701  
 TELEX: 846169  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 839 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-197-636-4

Query Match 39.2%; Score 1796; DB 4; Length 839;  
 Best Local Similarity 44.8%; Pred. No. 6.9e-159;  
 Matches 373; Conservative 156; Mismatches 223; Indels 81; Caps 15;

QY 49 PSPADSRPAGDGRNL-----RMKFGQ-----AFKGVNPIDLLS--TLVESSV 95  
 DB 22 PDLGDGPNRPAPQSTAKSRRLFQKGESEAFVDCPHEGELSCPTITVSPV 81  
 QY 96 V-----PGPKAPMDSLFDTYGRHSSDNKRWRKKIIEKQPSKAPAPQPPILKVF 149  
 DB 82 ITIORPCDGTGARL-----LSQDSVAASTEKTLRLY 113  
 QY 150 NRPILEDIVRGSTADLGLLPLTHKKRLTDEEPREPSTGKTCPLKALLNSGRNDT 209  
 DB 114 DRSIFEAVQNNCODLESLLFLQSKKHXTDNEFKDPETGKTKLLKAMLNLDGQNTT 173  
 QY 210 IPVLLDTAERTGNMREINSFPRDIYRGOTALHIAIERCKHYVELLVAGADVHAQAR 269  
 DB 174 IPLLLETARTDSLKELVNAXYTDXYKGTQALHIAIERRMALVTLVLLVENGADVOAAH 233  
 QY 270 GREFFQKDEGGYFYGELPLSLAACTNQPHIVNYLTENPHKKADMRQDSRGNTVLHALV 329  
 DB 234 GDFEKKTKRPGYFGEPLSLAACTNQLGIVKFLQNSQWADISARDSVGNVTVLHALV 293  
 QY 330 AIADNTRENTKFTVKYDLLLLLKKARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGTFQHI 389  
 DB 294 EVADNTADNTKFTSYMNEYILGAKLHPTLKLEELTNKKGMTPLAAGTGKIGVLAYI 353  
 QY 390 IREVDDETRHLSRKFQKWAYGPVYSSLYDLSLDTCGEASVLETLVY-NSK IENRHE 448  
 DB 354 LQREIOBPCRHLRSRAFTWAYGPVHSSLYDLSCIDTC-EKNSVLEVIAYSSSETPNRHD 412  
 QY 449 MLAVEPINELLRDKRKFQAVSFYINVVSYLCAWVIFTLTAYYQPLEGTPPYRYRTVDY 508  
 DB 413 MLLVEPLNRLLOQKWDREKRIEYFNFVLYCYLYIIFTMAAYYRPVLDGLPPFKMKTGDY 472

QY 509 LRLAGEVITLTGTGLFFFTNIKDLPMKKCPGVNSLFTDGSFQLLYFIYVSVLYVSAALYL 568  
 DB 473 FRVTGEILSLVGGYFFFRGIQ-YFLQRRPSMKTLFVDSYSEMLFFLQSLFMLATVVLVYF 531  
 QY 569 AGTEAYLAVVYFALVGLGMNALYFTGKLGKLTGYYSIMQKTLFKDLRFLLVLLFMWIGY 628  
 DB 532 SHLKEYVASWVSLALGWTNNLYYTRFGQMGYIYAVMIKWLRLDLRCRFMFVYVFLFGF 591  
 QY 629 ASALVSLNCPANMKVCNEDQTNCTVPTY-----PSCRDSET-----FSTFLDLDFK 675  
 DB 592 STAVVTLI-----EDGKNDLSPSESTSHRWGRGPACRPDPSSYNSLYST-CLELFFK 640  
 QY 676 LTGMGDLMLSSTKYPVFIILLVYIITFVLLNMLIALMGETVGVQVSKESKHVWL 735  
 DB 641 FTGMGDLTEFTENYDFKAVFIILLAYVILTYILLNMLIALMGETVYKIAQESKNVWL 700  
 QY 736 QWATTILDIERSFPVFLRKAPRSGEMVYVCKSGSDGTPDRRCFRVDEVNKSHNONGII 795  
 DB 701 ORAITILDTKSEFLKCMRKAFRSGKLLQVGYTPDGKDDYRWCFRVDEVNNTWNTNVGII 760  
 QY 796 NEDPGKNE-TYQYGFSTHTVGLRRDRWS--SVVPRVVELN---KNSNPDEV 841  
 DB 761 NEDPGNCEGVKRTLSPSLRSRVSGRHKNFALVPLLRASARDROSAQPEEV 813

## RESULT 12

US-09-235-451-4  
 ; Sequence 4, Application US/09235451  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Julius, David J.  
 ; APPLICANT: Caterina, Michael J.  
 ; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING  
 ; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED  
 ; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF  
 ; FILE REFERENCE: 9076/084CIP  
 ; CURRENT APPLICATION NUMBER: US/09/235,451  
 ; CURRENT FILING DATE: 1999-01-22  
 ; PRIOR APPLICATION NUMBER: 60/072,151  
 ; PRIOR FILING DATE: 1998-01-22  
 ; PRIOR APPLICATION NUMBER: 08/915,461  
 ; PRIOR FILING DATE: 1997-08-20  
 ; NUMBER OF SEQ ID NOS: 48  
 ; SOFTWARE: FASTSEQ for Windows Version 3.0  
 ; SEQ ID NO 4  
 ; LENGTH: 761  
 ; TYPE: PRT  
 ; ORGANISM: R. rattus  
 US-09-235-451-4

Query Match 32.7%; Score 1497.5; DB 4; Length 761;  
 Best Local Similarity 43.6%; Pred. No. 4.8e-131;  
 Matches 336; Conservative 123; Mismatches 247; Indels 65; Caps 14;  
 QY 103 PMDSLFDTYGRHSSDNKRWRKKIIEKQPSKAPAPQPPILKLVNRPILFDIVSRGS 162  
 DB 34 PMSFPQ--REDNRNSPQIKVNFIRKPPKNTSAPSOQEP---DRFDRDLFSVSVRGV 88  
 QY 163 TADLDGLLPLTHKKRLTDEEPREPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGN 222  
 DB 89 PELTGLLEVLWNYSKYLTDTSAYTEGSTGKTCMLKAVLNLODGVNACIMPLLDIDKDSGN 148  
 QY 223 MREIFNSPFDIYYRGOTALHIAIERCKHYVELLVAGADVHAQARGFQPKDEGGYF 282  
 DB 149 PKPLVNAQCTDEFYQGSALHIAIERKSLQCVKLLVENGADVHLRACGRFFQ-KHQCTCF 207  
 QY 283 YFCEPLSLAACTNQPHIVNYLTENPHKKADMRQDSRGNTVLHALVATADNTRKTFV 342  
 DB 208 YFCEPLSLAACTNQPHIVNYLTENPHQPSLASLEATDSLGNTVLHALVMADNSPENSALV 267  
 QY 343 TKMYDLLLLKCARLFPDSNLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDETRHL 402

Db 268 IHMYDGLQWGLARLCTVTOLEISNMQGLTPLKLAKEGKIEIFRHILOREFSG-PYOPL 326  
QY 403 SRKFKDWAYGVPYSSLYDLSSDTCGEASVLEILVYNSKIENRHEMLAVEPINELLROK 462  
Db 327 SRKFEMWCVPYVSYLDSSVDS-WEKNSVLEIIFAFCKSPRRHRMVLEPLNKLQEK 385  
QY 463 WRKFGAVSYINNVSYLCAMVITITAYQPLEGPPYP--YRTTVDYLRAGEVITLFT 520  
Db 386 WDRL-VSRFFNFACVLYVMFTTAVVHOPSLDQPAIPSSKATTFESMLLGHILILG 444  
QY 521 GV-----LFFFTNKLKFMKCPGVNSLFDIGSQLLFYISVLVIVSAALYLAGIEAY 574  
Db 445 GYLLGLQWYFWR-RRLF-----IWISFMDSYFEILFQALLTVLSQVLRMETEWY 497  
QY 575 LAVMYFALVGLWGNALYFTRGLKLTGTSIMQKILFKDLFRLLVLFMIGYASALS 634  
Db 498 LPLLVSLVGLWNLVYTRGFQHTGYISVMQKVLRLDLLFLLVYLVFGLGFAVALS 557  
QY 635 LNPCKANKVCNEDQTNCTVTPYPCRSRSETSTF-----LLDFKLTIGMDLEMS 688  
Db 558 LSREARSPKA--PEDNNSTVTEQPTVGQEEEPAPYRSILDALELFKFTIGMELAFQEQ 615  
QY 689 TRYPVFIILLVYIILFVLLNMLIALMGETVQVSKESKHINKLOWATTILDIERSF 748  
Db 616 LRFRGVULLLLAYVLLTYVLLNMLIALMSETVNHVADNSWSINKLOKASIVLEMENGY 675  
QY 749 PVFLKAPRSGEMVTVGKSSDGTDPDRWCFRVDEVNWSHWNONLGIINEDPG----- 800  
Db 676 WWCRRKKHREGLLKVGTRGDTGTPDRWCFRVEEVNWAAREKTLTSLSDPGSGITGNK 735  
QY 801 KNETYQYGFSTVGLRRDRWSSVYVVELNKNPNDEVVVPLDSMGNP 851  
Db 736 KNPT-----SKPGKNSASEDHLPLQVLQSP 761

## RESULT 13

US-09-132-316-2  
; Sequence 2, Application US/09132316B  
; Patent No. 6444440  
; GENERAL INFORMATION:  
; APPLICANT: Young, Paul E.  
; APPLICANT: Ruben, Steven M.  
; TITLE OF INVENTION: Vanilloid Receptor-2  
; FILE REFERENCE: 1488.1110000  
; CURRENT APPLICATION NUMBER: US/09/132,316B  
; CURRENT FILING DATE: 1998-08-11  
; EARLIER APPLICATION NUMBER: US 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 889  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-132-316-2

Query Match 32.2%; Score 1474.5; DB 4; Length 889;  
Best Local Similarity 41.4%; Pred. No. 8.8e-129;  
Matches 340; Conservative 118; Mismatches 258; Indels 105; Gaps 14;  
QY 20 GDESCTPGGEAFPLSSLANLEFEGDGLSPSPADASRAGP----- 60  
Db 94 GOHRRARKGTGTLTSPAQRSLWLDRAVPPPPRMTSPSSSPVRLTLDGGOEDGEADR 153  
QY 61 -----GDRPNLRMKFOCAFRKGVNPNIDLLESTLYESSVFGPKAPMDSLFYGVYRH 115  
Db 154 KGLDFGSLPWPESQFQEDRKFP----- 178  
QY 116 HSSDNKRWRKIIIEKQOSKAPAPQPPPIKLVFNRPILFDIVSRGSTADLDGLPFLIT 175  
Db 179 QIRVNLNRYK-----GTGASQDPD--NRDRDLRFNVAHSVGVPEDLAGLPEYLSK 226

QY 176 HKKRLTDEFRPSTGKTCPLKALLNSNGRNDTIPVLLDIAERTGNREFINSPPRDY 235  
Db 227 TSKYLTDSYTTSGTGKTCPLKAVLNKDCVACILPLLOIDRDSNPOPLVNAQCTDDY 286  
QY 236 YRGOTALHTAIERRCKHYVELLYVAOGADYHAQARFFQPKDEGGYFYFGEPLSLAACT 295  
Db 287 YRGHSALHTAIEKRSLOQCVKLVENGANCANVHARACGRFQ-KGGQTCFYFGEPLSLAACT 345  
QY 296 NQPHVNLVLTENPHKADMRRODSRGNTVHLVAVATADNTRENTKVTVMYDILLKLCAR 355  
Db 346 KQMDVVSYLLENPHOPASLOQATDSOGNTVHLVAVMISONSANALVTSYDGLLOAGAR 405  
QY 356 LFPDSNLEAVLNNDGLSPLMAAKTKIGIFQIIRREVTDTRHLSKFKDWAYGPVY 415  
Db 406 LCPVTOLEDIRNLQDLTPLKLAKEGKIEIFRHILOREFS--GLSHLSRKFTWCYGPVR 463  
QY 416 SLYDSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKRKFAGVSYINV 475  
Db 464 VSLYDLASVDSC-EENSVELEIIFAFCKSPRRHRMVVLEPLNKLQAKWDL-IPKFFLNF 521  
QY 476 VSYLCAMVITITAYQOP-LEGTTPPYRTTVDYLRAGEVITLFTGVLFFFFTNKKDLEM 534  
Db 522 LCNLYMFTTAVAHQPTLKAAPHLKAEVGNMMLTGHILILGGLYLLVQCLW-YEW 580  
QY 535 KPCPGVNSLFDIGSQLLFYISVLVIVSAALYLAGIEAYLAVMYFALVGLWGNALYFTR 594  
Db 581 RRVHVTWISFIDSYFEILFQALLTVVSOVLCFLAEIWEYLLVPLVLSALVGLWNLVYTR 640  
QY 595 GUKLTGTYSIMQKILFKDLFRLLVLFMIGYASALSLSLNPCKANKVCNEDQTNCTV 654  
Db 641 GFQHTGYISVMQKVLRLDLLFLLVYLVFGLGFAVALVSL-----SQEAMRPEA 690  
QY 655 PTPYPCRS-----ETPSTFL--LDLFKLTIGMDLEMLSTKYVYVFIIL 698  
Db 691 PTGPNATESVQPMQEGDEGNGAQVRLGILEASLELFTKFTIGMELAFQEQHFRGMVLLL 750  
QY 699 LVTYIILFVLLNMLIALMGETVQVSKESKHINKLOWATTILDIERSFPVFLRKAFRS 758  
Db 751 LLAYVLLTYVLLNMLIALMSETVNSVATDSINSINKLOKASIVLEMENGY-WWCRRKKQRA 809  
QY 759 GEMVTVGKSSDGTDPDRWCFRVDEVNWSHWNONLGIINEDP 799  
Db 810 GYMLTVGTRKPGSDPDRWCFRVEEVNWSWASQETLPTLCBDP 850

## RESULT 14

US-09-235-451-36  
; Sequence 36, Application US/09235451  
; GENERAL INFORMATION:  
; APPLICANT: Julius, David J.  
; APPLICANT: Caterina, Michael J.  
; APPLICANT: Brake, Anthony J.  
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING  
; TITLE OF INVENTION: CAPSAICIN RECEPTOR AND CAPSAICIN RECEPTOR-RELATED  
; TITLE OF INVENTION: POLYPEPTIDES AND USES THEREOF  
; FILE REFERENCE: 9076/084CIP  
; CURRENT APPLICATION NUMBER: US/09/235,451  
; CURRENT FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/072,151  
; PRIOR FILING DATE: 1998-01-22  
; PRIOR APPLICATION NUMBER: 08/915,461  
; PRIOR FILING DATE: 1997-08-20  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 36  
; LENGTH: 764  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-235-451-36

Query Match 32.1%; Score 1467; DB 4; Length 764;  
Best Local Similarity 43.1%; Pred. No. 3.5e-128;



Db 667 FRVEYNWASWEOTLPTLCEDP 688

Search completed: June 3, 2003, 19:56:29  
Job time : 23 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run On: June 3, 2003, 19:54:28 ; Search time 28 seconds  
(without alignments)  
3145.165 Million cell updates/sec

Title: US-09-870-090A-2

Perfect score: 4577

Sequence: 1 MADSSGPRAGPCEVAELPG.....PRCDGHQGYPRKWRDTPAD 870

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 383519 seqs, 101223694 residues

Total number of hits satisfying chosen parameters: 383519

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4573	99.9	871	9	US-10-027-828-4
2	4573	99.9	871	9	US-10-000-823-7
3	4571	99.9	871	9	US-10-027-828-2
4	4571	99.9	871	9	US-10-090-215-7
5	4546	99.3	871	9	US-10-227-255A-3
6	4378	95.7	871	9	US-10-027-828-11
7	4374	95.6	871	9	US-10-227-255A-1
8	4372	95.5	871	9	US-10-027-828-10
9	4371	95.5	871	9	US-10-027-828-8
10	4371	95.5	871	9	US-10-027-828-9
11	4334.5	94.7	870	9	US-10-027-828-13
12	4218	92.2	811	9	US-10-090-215-9
13	4199	91.7	803	10	US-09-764-367A-8
14	4138	90.4	792	10	US-09-764-367A-2
15	4127.5	90.2	830	9	US-10-027-828-6
16	3853	84.2	743	10	US-09-764-367A-11
17	3831.5	83.7	852	9	US-10-027-828-15
18	3829	83.7	742	9	US-10-090-215-12
19	3783.5	82.7	734	10	US-09-764-367A-4

20	2307	50.4	461	9	US-10-027-828-5	Sequence 5, Appli
21	2059.5	45.0	420	9	US-10-027-828-7	Sequence 7, Appli
22	1845.5	40.3	843	9	US-09-978-303-25	Sequence 25, Appl
23	1818	39.7	838	9	US-10-137-316-3	Sequence 3, Appli
24	1818	39.7	838	9	US-09-978-303-2	Sequence 2, Appli
25	1811.5	39.6	707	9	US-10-027-828-17	Sequence 17, Appli
26	1801	39.3	839	10	US-09-824-258-2	Sequence 2, Appli
27	1800	39.3	839	9	US-10-000-823-5	Sequence 5, Appli
28	1800	39.3	839	9	US-09-978-303-34	Sequence 34, Appli
29	1800	39.3	839	10	US-09-824-258-8	Sequence 8, Appli
30	1799	39.3	839	9	US-10-128-853-2	Sequence 2, Appli
31	1796	39.2	839	10	US-09-824-258-4	Sequence 4, Appli
32	1745	38.1	829	10	US-09-764-367A-7	Sequence 7, Appli
33	1497.5	32.7	761	9	US-09-978-303-4	Sequence 4, Appli
34	1474.5	32.2	889	9	US-10-137-316-2	Sequence 2, Appli
35	1467	32.1	764	9	US-10-000-823-6	Sequence 6, Appli
36	1467	32.1	764	9	US-09-978-303-36	Sequence 36, Appli
37	1467	32.1	764	10	US-09-828-466-4	Sequence 4, Appli
38	1459.5	31.9	665	9	US-10-027-828-18	Sequence 18, Appli
39	1454.5	31.8	764	10	US-09-828-466-5	Sequence 5, Appli
40	1445.5	31.6	790	9	US-10-011-582-6	Sequence 6, Appli
41	1438	31.4	761	9	US-10-011-582-10	Sequence 10, Appli
42	1436	31.4	760	10	US-09-764-367A-9	Sequence 9, Appli
43	1429.5	31.2	724	9	US-10-011-582-2	Sequence 2, Appli
44	1410.5	30.8	720	9	US-10-000-823-2	Sequence 2, Appli
45	1410.5	30.8	745	9	US-10-000-823-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-10-027-828-4

; Sequence 4, Application US/10027828

; Publication No. US20030013650A1

; GENERAL INFORMATION:

; APPLICANT: Liedtke, Wolfgang

; APPLICANT: Heller, Stefan

; APPLICANT: Hudspeth, Albert J.

; APPLICANT: Friedman, Jeffrey M.

; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC

; FILE OF INVENTION: IT, AND USES THEREOF

; FILE REFERENCE: 600-1-287N

; CURRENT FILING DATE: 2001-10-25

; PRIOR APPLICATION NUMBER: US/10/027,828

; PRIOR FILING DATE: 2000-10-26

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 871

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-027-828-4

Query Match 99.9% Score 4573; DB 9; Length 871;  
Best Local Similarity 99.9% Pred. No. 0;  
Matches 869; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MADSSGPRAGPCEVAELPGDESGT	PGGEAFPLSSLANLFE	GDGSLSPGADASR	PAGP 60
Db	1	MADSSGPRAGPCEVAELPGDESGT	PGGEAFPLSSLANLFE	GDGSLSPGADASR	PAGP 60
Qy	61	GDGRPNRMKFCQAFKRGVNP	IDLLESTLYESSVW	PGPKAPMDSLFD	GYGTYRHHSSDN 120
Db	61	GDGRPNRMKFCQAFKRGVNP	IDLLESTLYESSVW	PGPKAPMDSLFD	GYGTYRHHSSDN 120
Qy	121	KRWKTKTKKPOSPKAPAPQPP	ILKAVENRPI	LDVSRGSTADL	DGLLPFLTLTKKRL 180
Db	121	KRWKTKTKKPOSPKAPAPQPP	ILKAVENRPI	LDVSRGSTADL	DGLLPFLTLTKKRL 180
Qy	181	TDEEFREPTSGKTC	CLPKALLNLS	NGRNDTIPV	LLDIAERTGNMREFINSP
Db	181	TDEEFREPTSGKTC	CLPKALLNLS	NGRNDTIPV	LLDIAERTGNMREFINSP

Db 181 TDEFRPSTGKTCPLKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
 Qy 241 ALHTAIERCKHYVELLYVAQADYVAQARGFFQPKDEGGYFYFGELPLSLAACTNPHI 300  
 Db 241 ALHTAIERCKHYVELLYVAQADYVAQARGFFQPKDEGGYFYFGELPLSLAACTNPHI 300  
 Qy 301 VNYLTENPHKKADMRRODSRGNTVHLALVAIADNTRENTKFTVKMYDLKLLKCARLPDS 360  
 Db 301 VNYLTENPHKKADMRRODSRGNTVHLALVAIADNTRENTKFTVKMYDLKLLKCARLPDS 360  
 Qy 361 NLEAVLNNDGLSPLMAAKTGKIGIFOHIIIRREVTDEDTLRLSKRKFDMWAGPYVSSLYD 420  
 Db 361 NLEAVLNNDGLSPLMAAKTGKIGIFOHIIIRREVTDEDTLRLSKRKFDMWAGPYVSSLYD 420  
 Qy 421 LSSLDTCGEASVLEILVYNSKIENRHMLAVEPINELLRDKWRKFGAVSYINVSYLC 480  
 Db 421 LSSLDTCGEASVLEILVYNSKIENRHMLAVEPINELLRDKWRKFGAVSYINVSYLC 480  
 Qy 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFVFFFTNIDLFMKKCPGV 540  
 Db 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFVFFFTNIDLFMKKCPGV 540  
 Qy 541 NSLFIDGSFOLLFYIYSVLVIVSAALYLAGIEAYLAVMVFALVGLWMNLYFTFGLKLTG 600  
 Db 541 NSLFIDGSFOLLFYIYSVLVIVSAALYLAGIEAYLAVMVFALVGLWMNLYFTFGLKLTG 600  
 Qy 601 TYSIMIOKILFKDLFRLLYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 660  
 Db 601 TYSIMIOKILFKDLFRLLYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 660  
 Qy 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVYIILTFVLLNMLIALMGE 720  
 Db 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVYIILTFVLLNMLIALMGE 720  
 Qy 721 TVGVSKESKHINKLOWATTILDIERSFPVFLKRAFSGEMVTVGKSSDGTDPDRRCFRV 780  
 Db 721 TVGVSKESKHINKLOWATTILDIERSFPVFLKRAFSGEMVTVGKSSDGTDPDRRCFRV 780  
 Qy 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSTVGRRLDRRWSVVPVVELNKNPNDE 840  
 Db 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSTVGRRLDRRWSVVPVVELNKNPNDE 840  
 Qy 841 VVYPLDSMGNPRCDGHQGYPRKWRDADAP 870  
 Db 841 VVYPLDSMGNPRCDGHQGYPRKWRDADAP 870

## RESULT 2

us-10-000-823-7  
 ; Sequence 7, Application US/10000823  
 ; Publication No. US20030027164A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bristol-Myers Squibb Company  
 ; TITLE OF INVENTION: NOVEL HUMAN NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING A NO  
 ; TITLE OF INVENTION: HUMAN ION CHANNEL EXPRESSED IN SPINAL CORD AND BRAIN  
 ; FILE REFERENCE: D0109NP  
 ; CURRENT APPLICATION NUMBER: US/10/000,823  
 ; CURRENT FILING DATE: 2001-11-30  
 ; PRIOR APPLICATION NUMBER: 60/250,587  
 ; PRIOR FILING DATE: 2000-12-01  
 ; NUMBER OF SEQ ID NOS: 31  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 7  
 ; LENGTH: 871  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 us-10-000-823-7

Query Match 99.9%; Score 4573; DB 9; Length 871;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 869; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MADSEGPAGPGEVAELPGDESGTSGEAFPLSSLANLFEDEGSLSPSPADASRPAGP 60

Db 1 MADSEGPAGPGEVAELPGDESGTSGEAFPLSSLANLFEDEGSLSPSPADASRPAGP 60  
 Qy 61 GDGRPNLRMRKFOGAFRKGVNPNIDLLLESTLYESSVVPKPKAPMDSLFDYCTYRHSSDN 120  
 Db 61 GDGRPNLRMRKFOGAFRKGVNPNIDLLLESTLYESSVVPKPKAPMDSLFDYCTYRHSSDN 120  
 Qy 121 KRWRKKKIEKQPOSPKAPAPQPPPIKLVFNRPILFDIVSRGSTADLGLLPLFLTHKKRL 180  
 Db 121 KRWRKKKIEKQPOSPKAPAPQPPPIKLVFNRPILFDIVSRGSTADLGLLPLFLTHKKRL 180  
 Qy 181 TDEFRPSTGKTCPLKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
 Db 181 TDEFRPSTGKTCPLKALLNLSNGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
 Qy 241 ALHTAIERCKHYVELLYVAQADYVAQARGFFQPKDEGGYFYFGELPLSLAACTNPHI 300  
 Db 241 ALHTAIERCKHYVELLYVAQADYVAQARGFFQPKDEGGYFYFGELPLSLAACTNPHI 300  
 Qy 301 VNYLTENPHKKADMRRODSRGNTVHLALVAIADNTRENTKFTVKMYDLKLLKCARLPDS 360  
 Db 301 VNYLTENPHKKADMRRODSRGNTVHLALVAIADNTRENTKFTVKMYDLKLLKCARLPDS 360  
 Qy 361 NLEAVLNNDGLSPLMAAKTGKIGIFOHIIIRREVTDEDTLRLSKRKFDMWAGPYVSSLYD 420  
 Db 361 NLEAVLNNDGLSPLMAAKTGKIGIFOHIIIRREVTDEDTLRLSKRKFDMWAGPYVSSLYD 420  
 Qy 421 LSSLDTCGEASVLEILVYNSKIENRHMLAVEPINELLRDKWRKFGAVSYINVSYLC 480  
 Db 421 LSSLDTCGEASVLEILVYNSKIENRHMLAVEPINELLRDKWRKFGAVSYINVSYLC 480  
 Qy 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFVFFFTNIDLFMKKCPGV 540  
 Db 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFVFFFTNIDLFMKKCPGV 540  
 Qy 541 NSLFIDGSFOLLFYIYSVLVIVSAALYLAGIEAYLAVMVFALVGLWMNLYFTFGLKLTG 600  
 Db 541 NSLFIDGSFOLLFYIYSVLVIVSAALYLAGIEAYLAVMVFALVGLWMNLYFTFGLKLTG 600  
 Qy 601 TYSIMIOKILFKDLFRLLYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 660  
 Db 601 TYSIMIOKILFKDLFRLLYLLFMIGYASALVSLNPNCAVMKVCNEDQNTCTVPTPSC 660  
 Qy 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVYIILTFVLLNMLIALMGE 720  
 Db 661 RDSFTSTFLDLFKLTIGMDLEMLSTKYPVVFIIILVYIILTFVLLNMLIALMGE 720  
 Qy 721 TVGVSKESKHINKLOWATTILDIERSFPVFLKRAFSGEMVTVGKSSDGTDPDRRCFRV 780  
 Db 721 TVGVSKESKHINKLOWATTILDIERSFPVFLKRAFSGEMVTVGKSSDGTDPDRRCFRV 780  
 Qy 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSTVGRRLDRRWSVVPVVELNKNPNDE 840  
 Db 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSTVGRRLDRRWSVVPVVELNKNPNDE 840  
 Qy 841 VVYPLDSMGNPRCDGHQGYPRKWRDADAP 870  
 Db 841 VVYPLDSMGNPRCDGHQGYPRKWRDADAP 870

## RESULT 3

us-10-027-828-2  
 ; Sequence 2, Application US/10027828  
 ; Publication No. US20030013650A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liedtke, Wolfgang  
 ; APPLICANT: Heller, Stefan  
 ; APPLICANT: Hudspeeth, Albert J.  
 ; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC A  
 ; TITLE OF INVENTION: IT, AND USES THEREOF  
 ; FILE REFERENCE: 600-1-287N  
 ; CURRENT APPLICATION NUMBER: US/10/027,828



; CURRENT FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: US 60/243,568  
; PRIOR FILING DATE: 2000-10-26  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 871  
; TYPE: PR1  
; ORGANISM: Homo sapiens  
US-10-027-828-2

Query Match 99.9%; Score 4571; DB 9; Length 871;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 868; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADSEGPAGGVEALPGDESGTGGGEAPPLSSLANLFEDEGSLSPSPADASRAGP 60  
Db 1 MADSEGPAGGVEALPGDESGTGGGEAPPLSSLANLFEDEGSLSPSPADASRAGP 60  
Qy 61 GDGRPNLRMKFOGAFRGVNPIDLLESTLYESSVPGPKAPMDSLFYGYTHHSSDN 120  
Db 61 GDGRPNLRMKFOGAFRGVNPIDLLESTLYESSVPGPKAPMDSLFYGYTHHSSDN 120  
Qy 121 KRWKIIIEKQPOSPKAPAPQPPILKVFNRPLFDIVSRGSTADLGLLPLFLTHKKRL 180  
Db 121 KRWKIIIEKQPOSPKAPAPQPPILKVFNRPLFDIVSRGSTADLGLLPLFLTHKKRL 180  
Qy 181 TDEEFREPSGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
Db 181 TDEEFREPSGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
Qy 241 ALHAIERRCKHYVELLVAGADYHAQARGFFQPKDEGGYFYFGEPLSLAAGTNP 300  
Db 241 ALHAIERRCKHYVELLVAGADYHAQARGFFQPKDEGGYFYFGEPLSLAAGTNP 300  
Qy 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKVFVKMYDGLLLKCARLPDS 360  
Db 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKVFVKMYDGLLLKCARLPDS 360  
Qy 361 NLEAVLNDGLSPLMAAKTKIGIFOHIIIRREYTDTRHLSRKFWDYAGPVYSSLYD 420  
Db 361 NLEAVLNDGLSPLMAAKTKIGIFOHIIIRREYTDTRHLSRKFWDYAGPVYSSLYD 420  
Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWKKFGAVSFYINVS 480  
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWKKFGAVSFYINVS 480  
Qy 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDLMKKKCPGV 540  
Db 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDLMKKKCPGV 540  
Qy 541 NSLFIDGSLFLLYIYSVLVSAALYLAGTEAVLVAVFALVGLWGNALYFTGLKLTG 600  
Db 541 NSLFIDGSLFLLYIYSVLVSAALYLAGTEAVLVAVFALVGLWGNALYFTGLKLTG 600  
Qy 601 TYSIMIOKILFKDLFRLVYLLFMIGYASALVSLNPNCKMKNYCNEDQNTCTVPTPSC 660  
Db 601 TYSIMIOKILFKDLFRLVYLLFMIGYASALVSLNPNCKMKNYCNEDQNTCTVPTPSC 660  
Qy 661 RDSFTFTFLDLFKLTIGMDLEMLSTKYPVVFIILLVYIITFVLLNMLIALMGE 720  
Db 661 RDSFTFTFLDLFKLTIGMDLEMLSTKYPVVFIILLVYIITFVLLNMLIALMGE 720  
Qy 721 TVGQVSKESHIKLOWATILDIERSFPFLKAFRSGEMVTGKSSDGTDDRRCFRV 780  
Db 721 TVGQVSKESHIKLOWATILDIERSFPFLKAFRSGEMVTGKSSDGTDDRRCFRV 780  
Qy 781 DEVNWSHWNGLIINEDPKNETYQYGFSTYVGRLLRRDRSSWVPRVLELNKSNPDE 840  
Db 781 DEVNWSHWNGLIINEDPKNETYQYGFSTYVGRLLRRDRSSWVPRVLELNKSNPDE 840  
Qy 841 VVPLDMSGNPRCDGHOQGYPRKWRDADP 870  
VVPLDMSGNPRCDGHOQGYPRKWRDADP 870

Db 841 VVPLDMSGNPRCDGHOQGYPRKWRDADP 870

## RESULT 4

US-10-090-215-7  
; Sequence 7, Application US/10090215  
; Publication No. US20030032097A1  
; GENERAL INFORMATION:  
; APPLICANT: Dubin, Adrienne E  
; APPLICANT: Huvar, Arne  
; APPLICANT: Erlander, Mark G  
; APPLICANT: Glass, Charles A  
; TITLE OF INVENTION: DNA encoding isoforms of the human Vanilloid Receptor  
; FILE REFERENCE: Human VR3  
; CURRENT APPLICATION NUMBER: US/10/090.215  
; CURRENT FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 871  
; TYPE: PR1  
; ORGANISM: Homo sapiens  
US-10-090-215-7

Query Match 99.9%; Score 4571; DB 9; Length 871;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 869; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MADSEGPAGGVEALPGDESGTGGGEAPPLSSLANLFEDEGSLSPSPADASRAGP 60  
Db 1 MADSEGPAGGVEALPGDESGTGGGEAPPLSSLANLFEDEGSLSPSPADASRAGP 60  
Qy 61 GDGRPNLRMKFOGAFRGVNPIDLLESTLYESSVPGPKAPMDSLFYGYTHHSSDN 120  
Db 61 GDGRPNLRMKFOGAFRGVNPIDLLESTLYESSVPGPKAPMDSLFYGYTHHSSDN 120  
Qy 121 KRWKIIIEKQPOSPKAPAPQPPILKVFNRPLFDIVSRGSTADLGLLPLFLTHKKRL 180  
Db 121 KRWKIIIEKQPOSPKAPAPQPPILKVFNRPLFDIVSRGSTADLGLLPLFLTHKKRL 180  
Qy 181 TDEEFREPSGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
Db 181 TDEEFREPSGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
Qy 241 ALHAIERRCKHYVELLVAGADYHAQARGFFQPKDEGGYFYFGEPLSLAAGTNP 300  
Db 241 ALHAIERRCKHYVELLVAGADYHAQARGFFQPKDEGGYFYFGEPLSLAAGTNP 300  
Qy 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKVFVKMYDGLLLKCARLPDS 360  
Db 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKVFVKMYDGLLLKCARLPDS 360  
Qy 361 NLEAVLNDGLSPLMAAKTKIGIFOHIIIRREYTDTRHLSRKFWDYAGPVYSSLYD 420  
Db 361 NLEAVLNDGLSPLMAAKTKIGIFOHIIIRREYTDTRHLSRKFWDYAGPVYSSLYD 420  
Qy 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWKKFGAVSFYINVS 480  
Db 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWKKFGAVSFYINVS 480  
Qy 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDLMKKKCPGV 540  
Db 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDLMKKKCPGV 540  
Qy 541 NSLFIDGSLFLLYIYSVLVSAALYLAGTEAVLVAVFALVGLWGNALYFTGLKLTG 600  
Db 541 NSLFIDGSLFLLYIYSVLVSAALYLAGTEAVLVAVFALVGLWGNALYFTGLKLTG 600  
Qy 601 TYSIMIOKILFKDLFRLVYLLFMIGYASALVSLNPNCKMKNYCNEDQNTCTVPTPSC 660  
Db 601 TYSIMIOKILFKDLFRLVYLLFMIGYASALVSLNPNCKMKNYCNEDQNTCTVPTPSC 660  
Qy 661 RDSFTFTFLDLFKLTIGMDLEMLSTKYPVVFIILLVYIITFVLLNMLIALMGE 720  
Db 661 RDSFTFTFLDLFKLTIGMDLEMLSTKYPVVFIILLVYIITFVLLNMLIALMGE 720  
Qy 721 TVGQVSKESHIKLOWATILDIERSFPFLKAFRSGEMVTGKSSDGTDDRRCFRV 780  
Db 721 TVGQVSKESHIKLOWATILDIERSFPFLKAFRSGEMVTGKSSDGTDDRRCFRV 780  
Qy 781 DEVNWSHWNGLIINEDPKNETYQYGFSTYVGRLLRRDRSSWVPRVLELNKSNPDE 840  
Db 781 DEVNWSHWNGLIINEDPKNETYQYGFSTYVGRLLRRDRSSWVPRVLELNKSNPDE 840  
Qy 841 VVPLDMSGNPRCDGHOQGYPRKWRDADP 870  
VVPLDMSGNPRCDGHOQGYPRKWRDADP 870

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QY 661 RDSSTFSTFLDLFLKLTIGMGDLEMLSTKYPVVFIIILVYIIITFVLLNMLTALMG 720
DB 661 RDSSTFSTFLDLFLKLTIGMGDLEMLSTKYPVVFIIILVYIIITFVLLNMLTALMG 720
QY 721 TVGQVSKESKHIWKLOWATTILDIERSFPVFLKAFRSGEMVTGCKSSDGTDDRWCPRV 780
DB 721 TVGQVSKESKHIWKLOWATTILDIERSFPVFLKAFRSGEMVTGCKSSDGTDDRWCPRV 780
QY 781 DEVNWSHWNQNLGIINEDPGKNETYYGFGSHTVGLRRDRWSSVVPVVELNKNPNDE 840
DB 781 DEVNWSHWNQNLGIINEDPGKNETYYGFGSHTVGLRRDRWSSVVPVVELNKNPNDE 840
QY 841 VVPLDSMGNPRCDGHQOGYPRKWRRTDDAP 870
DB 841 VVPLDSMGNPRCDGHQOGYPRKWRRTDDAP 870

RESULT 5
US-10-227-255A-3
; Sequence 3, Application US/10227255A
; Publication No. US20030073117A1
; GENERAL INFORMATION:
; APPLICANT: Ishibashi, Ken'Ichi
; TITLE OF INVENTION: No. US20030073117A1el Protein and Gene Encoding the Protein
; FILE REFERENCE: 10969/2032
; CURRENT APPLICATION NUMBER: US/10/227,255A
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: PCT/JP01/01354
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP 048727/2000
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-227-255A-3

Query Match 99.3%; Score 4546; DB 9; Length 871;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 864; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MADSSEGPAGPGEVAELPGDESGTSGEAPFLSSLANLFEDEGSLSPSPADASRPPAG 60
DB 1 MADSSEGPAGPGEVAELPGDESGTSGEAPFLSSLANLFEDEGSLSPSPADASRPPAG 60
QY 61 GDRPNLRMKFQGAFRKGVNPNIDLESTLYESSVWPGPKAPMDSLFDYGYTHRHSSDN 120
DB 61 GDRPNLRMKFQGAFRKGVNPNIDLESTLYESSVWPGPKAPMDSLFDYGYTHRHSSDN 120
QY 121 KWRKKTIIEKQPSKPAPAPQPPILKVFNRPIILFVSRGSTADLGLLPFLTHKKRL 180
DB 121 KWRKKTIIEKQPSKPAPAPQPPILKVFNRPIILFVSRGSTADLGLLPFLTHKKRL 180
QY 181 TDEFPSTGKTCPLKALLNLSNGRNDTTPVLLDIAERTGNMREFINSPPRDIYYRGQT 240
DB 181 TDEFPSTGKTCPLKALLNLSNGRNDTTPVLLDIAERTGNMREFINSPPRDIYYRGQT 240
QY 241 ALHAIERRCKHYVELLVAOGADVHAQARGFFQPKDEGGYFYGELPLSLAACTNPQHI 300
DB 241 ALHAIERRCKHYVELLVAOGADVHAQARGFFQPKDEGGYFYGELPLSLAACTNPQHI 300
QY 301 VNYLTENPHKKADMRRODSRGNTVYLHALVAIAONTRENTKFTVKMYDLLLLKCARLPDS 360
DB 301 VNYLTENPHKKADMRRODSRGNTVYLHALVAIAONTRENTKFTVKMYDLLLLKCARLPDS 360
QY 361 NLEAVLNNDGLSPLMMAAKTGKIGFOHIIIRREVTDETRHLSRKKFKDWAYGPPYSSLYD 420
DB 361 NLEAVLNNDGLSPLMMAAKTGKIGFOHIIIRREVTDETRHLSRKKFKDWAYGPPYSSLYD 420
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSEYINVSYLC 480
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DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSEYINVSYLC 480
QY 481 AMWIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540
DB 481 AMWIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540
QY 541 NSLFDGSQLLYFIYSVLVIVSAALYLAGEIAYLAVMVFAVLGLGMMNALYFTRGLKLTG 600
DB 541 NSLFDGSQLLYFIYSVLVIVSAALYLAGEIAYLAVMVFAVLGLGMMNALYFTRGLKLTG 600
QY 601 TYSIMIQILFKDLFRFLLYLLFMIGYASALVSLNCPANKKVCNEDQTNCTVPTYPS 660
DB 601 TYSIMIQILFKDLFRFLLYLLFMIGYASALVSLNCPANKKVCNEDQTNCTVPTYPS 660
QY 661 RDSSTFSTFLDLFLKLTIGMGDLEMLSTKYPVVFIIILVYIIITFVLLNMLTALMG 720
DB 661 RDSSTFSTFLDLFLKLTIGMGDLEMLSTKYPVVFIIILVYIIITFVLLNMLTALMG 720
QY 721 TVGQVSKESKHIWKLOWATTILDIERSFPVFLKAFRSGEMVTGCKSSDGTDDRWCPRV 780
DB 721 TVGQVSKESKHIWKLOWATTILDIERSFPVFLKAFRSGEMVTGCKSSDGTDDRWCPRV 780
QY 781 DEVNWSHWNQNLGIINEDPGKNETYYGFGSHTVGLRRDRWSSVVPVVELNKNPNDE 840
DB 781 DEVNWSHWNQNLGIINEDPGKNETYYGFGSHTVGLRRDRWSSVVPVVELNKNPNDE 840
QY 841 VVPLDSMGNPRCDGHQOGYPRKWRRTDDAP 870
DB 841 VVPLDSMGNPRCDGHQOGYPRKWRRTDDAP 870

RESULT 6
US-10-027-828-11
; Sequence 11, Application US/10027828
; Publication No. US20030013650A1
; GENERAL INFORMATION:
; APPLICANT: Liedtke, Wolfgang
; APPLICANT: Heller, Stefan
; APPLICANT: Friedmann, Jeffrey M.
; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC A
; FILE REFERENCE: 600-1-287N
; CURRENT APPLICATION NUMBER: US/10/027,828
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,568
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-027-828-11

Query Match 95.7%; Score 4378; DB 9; Length 871;
Best Local Similarity 94.8%; Pred. No. 0;
Matches 825; Conservative 22; Mismatches 23; Indels 0; Gaps 0;

QY 1 MADSSEGPAGPGEVAELPGDESGTSGEAPFLSSLANLFEDEGSLSPSPADASRPPAG 60
DB 1 MADSSEGPAGPGEVAELPGDESGTSGEAPFLSSLANLFEDEGSLSPSPADASRPPAG 60
QY 61 GDRPNLRMKFQGAFRKGVNPNIDLESTLYESSVWPGPKAPMDSLFDYGYTHRHSSDN 120
DB 61 GDRPNLRMKFQGAFRKGVNPNIDLESTLYESSVWPGPKAPMDSLFDYGYTHRHSSDN 120
QY 121 KWRKKTIIEKQPSKPAPAPQPPILKVFNRPIILFVSRGSTADLGLLPFLTHKKRL 180
DB 121 KWRKKTIIEKQPSKPAPAPQPPILKVFNRPIILFVSRGSTADLGLLPFLTHKKRL 180
QY 181 TDEFPSTGKTCPLKALLNLSNGRNDTTPVLLDIAERTGNMREFINSPPRDIYYRGQT 240
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181 TDEEFREPSTGKTCPLKALLNLSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRQT 240
QY
241 ALHTAIERCKHYVELLVQAQADYHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300
Db
241 ALHTAIERCKHYVELLVQAQADYHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300
QY
301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKVTWKYDMLLLKLCARLPDPS 360
Db
301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKVTWKYDMLLLKLCARLPDPS 360
QY
361 NLEAVLNNDGLSPMLMAAKTGKIGIFQHIIRREVTDERTHLSRKFKDWAYGVPVSSLYD 420
Db
361 NLEAVLNNDGLSPMLMAAKTGKIGIFQHIIRREVTDERTHLSRKFKDWAYGVPVSSLYD 420
QY
421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRKWKFKGAVSYINVSYLE 480
Db
421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRKWKFKGAVSYINVSYLE 480
QY
481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540
Db
481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540
QY
541 NSLFDGSGFQLLYFYISVLVSAALYLAGIAYLAVMVFALVGLWMNALYFTRGLKLTG 600
Db
541 NSLFDGSGFQLLYFYISVLVSAALYLAGIAYLAVMVFALVGLWMNALYFTRGLKLTG 600
QY
601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVLLNPNCAKMKVCNEDQTNCTVPTPSC 660
Db
601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVLLNPNCAKMKVCNEDQTNCTVPTPSC 660
QY
661 RDSETFTFLDLFKLTIGMDLEMLSSAKYPPVVFILLVYIILFTVLLNMLIALMGE 720
Db
661 RDSETFTFLDLFKLTIGMDLEMLSSAKYPPVVFILLVYIILFTVLLNMLIALMGE 720
QY
721 TVGOVSKESKHIWKLQWATTILDIERSPFVFLKAFRSGEMVTYVKSDDGTPDRRWCFRV 780
Db
721 TVGOVSKESKHIWKLQWATTILDIERSPFVFLKAFRSGEMVTYVKSDDGTPDRRWCFRV 780
QY
781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSGHTVGLRRDRRWSSVVPVVELNKNPNDE 840
Db
781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSGHTVGLRRDRRWSSVVPVVELNKNPNDE 840
QY
841 VVPLDLSMGNPCDGHQOGYAPKWRDADAP 870
Db
841 VVPLDNLGNPCDGHQOGYAPKWRADAP 870
```

## RESULT 7

```

US-10-227-255A-1
; Sequence 1, Application US/10227255A
; Publication No. US20030073117A1
; GENERAL INFORMATION:
; APPLICANT: Suzuki, Makoto
; APPLICANT: Ishibashi, Ken'ichi
; TITLE OF INVENTION: No. US20030073117A1el Protein and Gene Encoding the Protein
; FILE REFERENCE: 10969/2032
; CURRENT APPLICATION NUMBER: US/10/227,255A
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: PCT/JP01/01354
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP 048727/2000
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-227-255A-1

Query Match          95.6%; Score 4374; DB 9; Length 871;
Best Local Similarity 94.8%; Pred. No. 0;
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```

Matches 825; Conservative 22; Mismatches 23; Indels 0; Gaps 0;
QY 1 MADSEPRACPGGEVAELPGDESGTSGGEAPLSSLANLFEGEDGLSPSPADASRRPAGP 60
Db 1 MADPGDGPRAAPGEVAEPDDESGTSGGEAPLSSLANLFEGEDGLSPSPADASRRPAGP 60
QY 61 GDGRPNLRMKFQGAFAKGVNPNIDLLESTLYESSVVGPKKAPMDLSLDYGYRHHSSDN 120
Db 61 GDGRPNLRMKFQGAFAKGVNPNIDLLESTLYESSVVGPKKAPMDLSLDYGYRHHSSDN 120
QY 121 KRWKRIIEKQFQSPKAPAPOPPPILKVFNPILFDIVSRGSTADLDGLLFLTHKKRL 180
Db 121 KRWKRVYVEKQFQSPKAPAPOPPPILKVFNPILFDIVSRGSTADLDGLLFLTHKKRL 180
QY 181 TDEEFREPSTGKTCPLKALLNLSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRQT 240
Db 181 TDEEFREPSTGKTCPLKALLNLSGRNDTIPVLLDIAERTGNMREFINSFPRDIYRQT 240
QY 241 ALHTAIERCKHYVELLVQAQADYHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300
Db 241 SLHTAIERCKHYVELLVQAQADYHAQARGFFQPKDEGGYFYFGEPLSLAACTNQPHI 300
QY 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKVTWKYDMLLLKLCARLPDPS 360
Db 301 VNYLTENPHKKADMRQDSRGNTVLHALVAIADNTRENTKVTWKYDMLLLKLCARLPDPS 360
QY 361 NLEAVLNNDGLSPMLMAAKTGKIGIFQHIIRREVTDERTHLSRKFKDWAYGVPVSSLYD 420
Db 361 NLEAVLNNDGLSPMLMAAKTGKIGIFQHIIRREVTDERTHLSRKFKDWAYGVPVSSLYD 420
QY 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRKWKFKGAVSYINVSYLE 480
Db 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRKWKFKGAVSYINVSYLE 480
QY 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540
Db 481 AMVIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFEEFTNIKDLFMKKCPGV 540
QY 541 NSLFDGSGFQLLYFYISVLVSAALYLAGIAYLAVMVFALVGLWMNALYFTRGLKLTG 600
Db 541 NSLFDGSGFQLLYFYISVLVSAALYLAGIAYLAVMVFALVGLWMNALYFTRGLKLTG 600
QY 601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVLLNPNCAKMKVCNEDQTNCTVPTPSC 660
Db 601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVLLNPNCAKMKVCNEDQTNCTVPTPAC 660
QY 661 RDSETFTFLDLFKLTIGMDLEMLSSAKYPPVVFILLVYIILFTVLLNMLIALMGE 720
Db 661 RDSETFTFLDLFKLTIGMDLEMLSSAKYPPVVFILLVYIILFTVLLNMLIALMGE 720
QY 721 TVGOVSKESKHIWKLQWATTILDIERSPFVFLKAFRSGEMVTYVKSDDGTPDRRWCFRV 780
Db 721 TVGOVSKESKHIWKLQWATTILDIERSPFVFLKAFRSGEMVTYVKSDDGTPDRRWCFRV 780
QY 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSGHTVGLRRDRRWSSVVPVVELNKNPNDE 840
Db 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSGHTVGLRRDRRWSSVVPVVELNKNPNDE 840
QY 841 VVPLDLSMGNPCDGHQOGYAPKWRDADAP 870
Db 841 VVPLDNLGNPCDGHQOGYAPKWRDADAP 870
```

## RESULT 8

```

US-10-027-828-10
; Sequence 10, Application US/10027828
; Publication No. US20030013650A1
; GENERAL INFORMATION:
; APPLICANT: Liedtke, Wolfgang
; APPLICANT: Heller, Stefan
; APPLICANT: Hudspeith, Albert J.
; APPLICANT: Friedman, Jeffrey M.
; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC
```

; TITLE OF INVENTION: IT, AND USES THEREOF
; FILE REFERENCE: 600-1-287N
; CURRENT APPLICATION NUMBER: US/10/027,828
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,568
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-10-027-828-10

Query Match 95.5%; Score 4372; DB 9; Length 871;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 824; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

QY 1 MADSSGPRAGGCEVAELPGDESGTPGGEAFPLSSLANLFEDEGSLSPDASRPAGP 60
Db 1 MADPGDGPRAAPGDAEPGDESGTSGGEAFPLSSLANLFEDEGSSLSPPVDASRPAGP 60
QY 61 GGRPNLNRMKFOGAFKGVNPNIDLLESTLYESSVVPKPKAPMDSLDPDYGYRRHSSDN 120
Db 61 GGRPNLNRMKFOGAFKGVNPNIDLLESTLYESSVVPKPKAPMDSLDPDYGYRRHPSDN 120
QY 121 KWRKKIIEKQSPKAPAPQPPILKVNRPILFDIVSRGSTADLDGLLTHKKRL 180
Db 121 KWRKKVVEKQSPKAPAPQPPILKVNRPILFDIVSRGSTADLDGLLTHKKRL 180
QY 181 TDEEREPSTGKTCLPKALLNLSNRNDTIPVLLDIAERTGNMREFINSPPRDIIYRGOT 240
Db 181 TDEEREPSTGKTCLPKALLNLSNRNDTIPVLLDIAERTGNMREFINSPPRDIIYRGOT 240
QY 241 ALHIAIERCKHYVELLVAQADVHAQAGRFQPKDEGGYFYFGEPLSLAACTNPHI 300
Db 241 ALHIAIERCKHYVELLVAQADVHAQAGRFQPKDEGGYFYFGEPLSLAACTNPHI 300
QY 301 VNYLTENPHKKADMRRQDSRGNTVYLHALVAIADNTRENTKFTVMYDLLLLKCARLPDS 360
Db 301 VNYLTENPHKKADMRRQDSRGNTVYLHALVAIADNTRENTKFTVMYDLLLLKCSRLFPDS 360
QY 361 NLEAVLNNDGLSPLMMAAKTGIGIFQHIIRREVTDERTHLRKRKOWAYGPVYSSLYD 420
Db 361 NLEAVLNNDGLSPLMMAAKTGIGIFQHIIRREVTDERTHLRKRKOWAYGPVYSSLYD 420
QY 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
Db 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
QY 481 AMVIFTLTAYQPLEGTPPYRTTVYDLRLAGEVITLTGVLFFFTNIKDLFMKKCPGV 540
Db 481 AMVIFTLTAYQPLEGTPPYRTTVYDLRLAGEVITLTGVLFFFTNIKDLFMKKCPGV 540
QY 541 NSLFDGSGFOLLFYIYSLVIVSAALYLAGIEAYLAVMVFAVLVGMNALLYFTRGLKLTG 600
Db 541 NSLFDGSGFOLLFYIYSLVIVSAALYLAGIEAYLAVMVFAVLVGMNALLYFTRGLKLTG 600
QY 601 TYSIMQIKFLKDLFRFLVLLFMIGYASALVSLNPNCAKMKVNEQDQNTCTVPTPSC 660
Db 601 TYSIMQIKFLKDLFRFLVLLFMIGYASALVTLNPNCTNMKVCNEQDQNTCTVPSYAC 660
QY 661 RDSFTSFLLDLFLKLTGMGDMLSSTKYPVWFIIILVTVIILTFVLLNMLALMGE 720
Db 661 RDSFTSFALLDLFLKLTGMGDMLSSTKYPVWFIIILVTVIILTFVLLNMLALMGE 720
QY 721 TVGOVSKESKHILKQWATTIILDIERSFPVLRKAFRSGEMVTGKSSDGTDRWCFCRV 780
Db 721 TVGOVSKESKHILKQWATTIILDIERSFPVLRKAFRSGEMVTGKSSDGTDRWCFCRV 780
QY 781 DEVNWSHWNQNLGIINEDPGKNETYYQYGFSTHGTGRLRRDRWSSVVPVWELNKNNSPDE 840
Db 781 DEVNWSHWNQNLGIINEDPGKSEIYYQYGFSTHGTGRLRRDRWSSVVPVWELNKNNSGTDE 840

QY 841 VVYPLDSMGNPRCDGHQGYPRKWRRTDDAP 870
Db 841 VVYPLDNLGNPNCDGHQGYAPKWRADAP 870

RESULT 9
US-10-027-828-8
; Sequence 8, Application US/10027828
; Publication No. US20030013650A1
; GENERAL INFORMATION:
; APPLICANT: Liedtke, Wolfgang
; APPLICANT: Heller, Stefan
; APPLICANT: Hudspeth, Albert J.
; APPLICANT: Friedman, Jeffrey M.
; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC
; FILE REFERENCE: 600-1-287N
; CURRENT APPLICATION NUMBER: US/10/027,828
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,568
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-10-027-828-8

Query Match 95.5%; Score 4371; DB 9; Length 871;
Best Local Similarity 94.7%; Pred. No. 0;
Matches 824; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

QY 1 MADSSGPRAGGCEVAELPGDESGTPGGEAFPLSSLANLFEDEGSLSPDASRPAGP 60
Db 1 MADPGDGPRAAPGDAEPGDESGTSGGEAFPLSSLANLFEDEGSSLSPPVDASRPAGP 60
QY 61 GGRPNLNRMKFOGAFKGVNPNIDLLESTLYESSVVPKPKAPMDSLDPDYGYRRHSSDN 120
Db 61 GGRPNLNRMKFOGAFKGVNPNIDLLESTLYESSVVPKPKAPMDSLDPDYGYRRHPSDN 120
QY 121 KWRKKIIEKQSPKAPAPQPPILKVNRPILFDIVSRGSTADLDGLLTHKKRL 180
Db 121 KWRKKVVEKQSPKAPAPQPPILKVNRPILFDIVSRGSTADLDGLLTHKKRL 180
QY 181 TDEEREPSTGKTCLPKALLNLSNRNDTIPVLLDIAERTGNMREFINSPPRDIIYRGOT 240
Db 181 TDEEREPSTGKTCLPKALLNLSNRNDTIPVLLDIAERTGNMREFINSPPRDIIYRGOT 240
QY 241 ALHIAIERCKHYVELLVAQADVHAQAGRFQPKDEGGYFYFGEPLSLAACTNPHI 300
Db 241 ALHIAIERCKHYVELLVAQADVHAQAGRFQPKDEGGYFYFGEPLSLAACTNPHI 300
QY 301 VNYLTENPHKKADMRRQDSRGNTVYLHALVAIADNTRENTKFTVMYDLLLLKCARLPDS 360
Db 301 VNYLTENPHKKADMRRQDSRGNTVYLHALVAIADNTRENTKFTVMYDLLLLKCSRLFPDS 360
QY 361 NLEAVLNNDGLSPLMMAAKTGIGIFQHIIRREVTDERTHLRKRKOWAYGPVYSSLYD 420
Db 361 NLEAVLNNDGLSPLMMAAKTGIGIFQHIIRREVTDERTHLRKRKOWAYGPVYSSLYD 420
QY 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
Db 421 LSSLDTCGEEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480
QY 481 AMVIFTLTAYQPLEGTPPYRTTVYDLRLAGEVITLTGVLFFFTNIKDLFMKKCPGV 540
Db 481 AMVIFTLTAYQPLEGTPPYRTTVYDLRLAGEVITLTGVLFFFTNIKDLFMKKCPGV 540
QY 541 NSLFDGSGFOLLFYIYSLVIVSAALYLAGIEAYLAVMVFAVLVGMNALLYFTRGLKLTG 600
Db 541 NSLFDGSGFOLLFYIYSLVIVSAALYLAGIEAYLAVMVFAVLVGMNALLYFTRGLKLTG 600

QY 601 TYSIMIOKILFKDLFRELVLVLLFMIGYASALVLLNPNCAKMKVCNEDQTNCTVPTYPSC 660.  
DB 601 TYSIMIOKILFKDLFRELVLVLLFMIGYASALVLLNPNCTNMKVCNEDQSNCTVPSYPAC 660  
QY 661 RDSFTSTFLDLFKLIGMGDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720  
DB 661 RDSFTSAFLDLFKLIGMGDLEMLSSAKYPVVFILLVYIILTFVLLNMLIALMGE 720  
QY 721 TVGQVSKESKHIKLOWATTILDIERSFPVFLKAFRSGEMVTYKSSDGTDDRWCFRV 780  
DB 721 TVGQVSKESKHIKLOWATTILDIERSFPVFLKAFRSGEMVTYKSSDGTDDRWCFRV 780  
QY 781 DEVNWSHWNQNLGIINEDPGKNETYYGYGFSHTVGRLLRRDRWSSVPRVVELNKNPNDE 840  
DB 781 DEVNWSHWNQNLGIINEDPGKSEIYYGYGFSHTMGLRRDRWSSVPRVVELNKNSGTDE 840  
QY 841 VVPLDSMGNPRCDGHOOGYPRKWRDADAP 870  
DB 841 VVPLDLNLPNCNCDGHOOGYAPKWRADAP 870

## RESULT 10

US-10-027-828-9

; Sequence 9, Application US/10027828

; Publication No. US20030013650A1

; GENERAL INFORMATION:

; APPLICANT: Liedtke, Wolfgang

; APPLICANT: Heller, Stefan

; APPLICANT: Hudspeth, Albert J.

; APPLICANT: Friedman, Jeffrey M.

; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC ACIDS

; FILE REFERENCE: 600-1-287N

; CURRENT APPLICATION NUMBER: US/10/027,828

; PRIOR FILING DATE: 2001-10-25

; PRIOR APPLICATION NUMBER: US 60/243,568

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 9

; LENGTH: 871

; TYPE: PRT

; ORGANISM: Rattus norvegicus

US-10-027-828-9

Query Match 95.58; Score 4371; DB 9; Length 871;

Best Local Similarity 94.7%; Pred. No. 0;

Matches 824; Conservative 22; Mismatches 24; Indels 0; Gaps 0;

QY 1 MADSGEPGAGGVAELPDGSGTSGEAFPLSSLANLFEDEGSLSPADASRRPAG 60

DB 1 MADPGDGPRAAGVADGVAEPDGSCTSGEAFPLSSLANLFEDEGSSSLSPVDASRRPAG 60

QY 61 GDGRPNLRMKFOGAFRGKVPNPIDLLESTLYESSVVPKPKAPMDSLFYGYTRHHSSDN 120

DB 61 GDGRPNLRMKFOGAFRGKVPNPIDLLESTLYESSVVPKPKAPMDSLFYGYTRHHSSDN 120

QY 121 KRWKPKKIEQPSKAPAPQPPPIKVFNRPIFLDIVSRGSTADLGLPLFLTHKKRL 180

DB 121 KRWKPKKIEQPSKAPAPQPPPIKVFNRPIFLDIVSRGSTADLGLPLFLTHKKRL 180

QY 181 TDEFRPSPGKTKLCPKALLNSGRNDTIPVLDDIAERTGNMREFINSFRDIYRGQT 240

DB 181 TDEFRPSPGKTKLCPKALLNSGRNDTIPVLDDIAERTGNMREFINSFRDIYRGQT 240

QY 241 ALHIAIERCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGELPLSLAACTNPHI 300

DB 241 ALHIAIERCKHYVELLVAQADVHAQARGFFQPKDEGGYFYFGELPLSLAACTNPHI 300

QY 301 VNYLTENPHKADMRRODSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLPDS 360

DB 301 VNYLTENPHKADMRRODSRGNTVLHALVAIADNTRENTKFTVMYDLLLLKCARLPDS 360

QY 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDRHLSKRFKDMAYGVPVYSSLYD 420  
DB 361 NLEAVLNNDGLSPLMMAAKTGKIGIFQHIIRREVTDEDRHLSKRFKDMAYGVPVYSSLYD 420  
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSEYINNVSYLC 480  
DB 421 LSSLDTCGEESVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSEYINNVSYLC 480  
QY 481 AMVIFTTATYQPLEGTPPYRTVDYLRAGEVITLFTGVLFFFTNIKDLFKMKKCPGV 540  
DB 481 AMVIFTTATYQPLEGTPPYRTVDYLRAGEVITLFTGVLFFFTNIKDLFKMKKCPGV 540  
QY 541 NSLFDGSGFOLLFYIYSVLVTSAAALYLAGIEAYLAVMVFALVGLGMNALLYFTRGKLKLTG 600  
DB 541 NSLFDGSGFOLLFYIYSVLVTSAAALYLAGIEAYLAVMVFALVGLGMNALLYFTRGKLKLTG 600  
QY 601 TYSIMIOKILFKDLFRELVLVLLFMIGYASALVLLNPNCAKMKVCNEDQTNCTVPTYPSC 660  
DB 601 TYSIMIOKILFKDLFRELVLVLLFMIGYASALVLLNPNCTNMKVCNEDQSNCTVPSYPAC 660  
QY 661 RDSFTSTFLDLFKLIGMGDLEMLSTKYPVVFILLVYIILTFVLLNMLIALMGE 720  
DB 661 RDSFTSAFLDLFKLIGMGKLEMLSSAKYPVVFILLVYIILTFVLLNMLIALMGE 720  
QY 721 TVGQVSKESKHIKLOWATTILDIERSFPVFLKAFRSGEMVTYKSSDGTDDRWCFRV 780  
DB 721 TVGQVSKESKHIKLOWATTILDIERSFPVFLKAFRSGEMVTYKSSDGTDDRWCFRV 780  
QY 781 DEVNWSHWNQNLGIINEDPGKNETYYGYGFSHTVGRLLRRDRWSSVPRVVELNKNPNDE 840  
DB 781 DEVNWSHWNQNLGIINEDPGKSEIYYGYGFSHTMGLRRDRWSSVPRVVELNKNSGTDE 840  
QY 841 VVPLDSMGNPRCDGHOOGYPRKWRDADAP 870  
DB 841 VVPLDLNLPNCNCDGHOOGYAPKWRADAP 870

## RESULT 11

US-10-027-828-13

; Sequence 13, Application US/10027828

; Publication No. US20030013650A1

; GENERAL INFORMATION:

; APPLICANT: Liedtke, Wolfgang

; APPLICANT: Heller, Stefan

; APPLICANT: Hudspeth, Albert J.

; APPLICANT: Friedman, Jeffrey M.

; TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC

; FILE REFERENCE: 600-1-287N

; CURRENT APPLICATION NUMBER: US/10/027,828

; PRIOR FILING DATE: 2001-10-25

; PRIOR APPLICATION NUMBER: US 60/243,568

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 13

; LENGTH: 870

; TYPE: PRT

; ORGANISM: Mus musculus

US-10-027-828-13

Query Match 94.7%; Score 4334.5; DB 9; Length 870;

Best Local Similarity 94.4%; Pred. No. 0;

Matches 821; Conservative 21; Mismatches 27; Indels 1; Gaps 1;

QY 1 MADSGEPGAGGVAELPDGSGTSGEAFPLSSLANLFEDEGSLSPADASRRPAG 60

DB 1 MADPGDGPRAAGVADGVAEPDGSCTSGEAFPLSSLANLFEDEGSSSLSPVDASRRPAG 60

QY 61 GDGRPNLRMKFOGAFRGKVPNPIDLLESTLYESSVVPKPKAPMDSLFYGYTRHHSSDN 120

DB 61 GDGRPNLRMKFRSAFRGKVPNPIDLLESTLYESSVVPKPKAPMDSLFYGYTRHHSSDN 120

QY 121 KWRKKIIEKQSPKAPAPQPPPIIKVFNRPILFDIVSRGSTADLDGLLFLTHKKRL 180  
DB 121 KWRKKVVEKQSPKAPAPQPPPIIKVFNRPILFDIVSRGSTADLDGLLFLTHKKRL 180  
QY 181 TDEEFPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240  
DB 181 TDEEFPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240  
QY 241 ALHIAIERCKHYVELLVAOGADVHAQARGFQPKDEGGYFYEGELPLSLAACTNPHI 300  
DB 241 SLHIAIERCKHYVELLVAOGADVHAQARGFQPKDEGGYFYEGELPLSLAACTNPHI 300  
QY 301 VNYLTENPHKKADMRQDSRGNTVYLHALVAIADTNTRENTKFTVMYDILLKLCARLPDS 360  
DB 301 VNYLTENPHKKADMRQDSRGNTVYLHALVAIADTNTRENTKFTVMYDILLKLCARLPDS 360  
QY 361 NLEAVLNNDGLSPLMAAKTGKIGIFQHIIRREVTDTRHLSRKFQKDMAYGPVYSYLD 420  
DB 361 NLEAVLNNDGLSPLMAAKTGKIGIFQHIIRREVTDTRHLSRKFQKDMAYGPVYSYLD 420  
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLEC 480  
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLEC 480  
QY 481 AMWIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDLPKMKCPGV 540  
DB 481 AMWIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDLPKMKCPGV 540  
QY 541 NSLFDGSGFQLLYFIYSVLVSAALYLAGEAYLAVVFAVLVGNMNLFTYRGLKLTG 600  
DB 541 NSLFDGSGFQLLYFIYSVLVSAALYLAGEAYLAVVFAVLVGNMNLFTYRGLKLTG 600  
QY 601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVSLNLANPCANMKVCNEDQTNCTVPTPSC 660  
DB 601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVSLNLANPCANMKVCNEDQTNCTVPTPAC 660  
QY 661 RDSFTFTFLDLFKLTIGMDLEMLSTKYPVVFIIILTYIILTFVLLNMLIALMGE 720  
DB 661 RDSFTFAFLDLFKLTIGMDLEMLSSAKYPVVFIIILTYIILTFVLLNMLIALMGE 720  
QY 721 TVGQVSKESKHIWKLOWATTIILDIERSFPVFLRAFRSGEMVTYVGSDDGTPDRRCFRV 780  
DB 721 TVGQVSKESKHIWKLOWATTIILDIERSFPVFLRAFRSGEMVTYVGSDDGTPDRRCFRV 780  
QY 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSGHTVGLRRDRWSSVPRVVELNKNKNPDE 840  
DB 781 DEVNWSHWNQNLGIINEDPG-SEIYQYGFSGHTVGLRRDRWSSVPRVVELNKNSSADE 839  
QY 841 VVPLDSMGNPCDGHQOQYPRKWRITDAP 870  
DB 840 VVPLDLNLPNCDDGHQOQYAPKWRITDAP 869

## RESULT 12

US-10-090-215-9

; Sequence 9, Application US/10090215

; Publication No. US20030032097A1

; GENERAL INFORMATION:

; APPLICANT: Dublin, Adrienne E

; APPLICANT: Huvar, Arne

; APPLICANT: Erlander, Mark G

; APPLICANT: Glass, Charles A

; TITLE OF INVENTION: DNA encoding isoforms of the human Vanilloid Receptor

; FILE REFERENCE: Human VR3 receptors

; CURRENT APPLICATION NUMBER: US/10/090.215

; CURRENT FILING DATE: 2002-03-04

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 811

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-090-215-9

Query Match 92.2%; Score 4218; DB 9; Length 811;

Best Local Similarity 93.0%; Pred. No. 0;

Matches 809; Conservative 0; Mismatches 1; Indels 60; Gaps 1;

QY 1 MADSEGPAGGVAELPGDESGTGGGAAPPLSLANLFEDEGSLSPSPADASRRPAGP 60  
DB 1 MADSEGPAGGVAELPGDESGTGGGAAPPLSLANLFEDEGSLSPSPADASRRPAGP 60  
QY 61 GDGPNLRMKFGQAFKGVNPNIDLLSTLYESSVVPCKKAPMDSLFDYGTYYRHSSDN 120  
DB 61 GDGPNLRMKFGQAFKGVNPNIDLLSTLYESSVVPCKKAPMDSLFDYGTYYRHSSDN 120  
QY 121 KWRKKIIEKQSPKAPAPQPPPIIKVFNRPILFDIVSRGSTADLDGLLFLTHKKRL 180  
DB 121 KWRKKIIEKQSPKAPAPQPPPIIKVFNRPILFDIVSRGSTADLDGLLFLTHKKRL 180  
QY 181 TDEEFPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240  
DB 181 TDEEFPSTGKTCPLKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOT 240  
QY 241 ALHIAIERCKHYVELLVAOGADVHAQARGFQPKDEGGYFYEGELPLSLAACTNPHI 300  
DB 241 ALHIAIERCKHYVELLVAOGADVHAQARGFQPKDEGGYFYEGELPLSLAACTNPHI 300  
QY 301 VNYLTENPHKKADMRQDSRGNTVYLHALVAIADTNTRENTKFTVMYDILLKLCARLPDS 360  
DB 301 VNYLTENPHKKADMRQDSRGNTVYLHALVAIADTNTRENTKFTVMYDILLKLCARLPDS 360  
QY 361 NLEAVLNNDGLSPLMAAKTGKIGIFQHIIRREVTDTRHLSRKFQKDMAYGPVYSYLD 420  
DB 361 NLEAVLNNDGLSPLMAAKTGKIGIFQHIIRREVTDTRHLSRKFQKDMAYGPVYSYLD 420  
QY 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLEC 480  
DB 421 LSSLDTCGEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSYLEC 480  
QY 481 AMWIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDLPKMKCPGV 540  
DB 481 AMWIFTLTAYQPLEGTPPYRTVDYLRAGEVITLFTGVLFNFKDLPKMKCPGV 540  
QY 541 NSLFDGSGFQLLYFIYSVLVSAALYLAGEAYLAVVFAVLVGNMNLFTYRGLKLTG 600  
DB 541 NSLFDGSGFQLLYFIYSVLVSAALYLAGEAYLAVVFAVLVGNMNLFTYRGLKLTG 600  
QY 601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVSLNLANPCANMKVCNEDQTNCTVPTPSC 660  
DB 601 TYSIMIOKILFKDLFRLLVYLLFMIGYASALVSLNLANPCANMKVCNEDQTNCTVPTPSC 660  
QY 661 RDSFTFTFLDLFKLTIGMDLEMLSTKYPVVFIIILTYIILTFVLLNMLIALMGE 720  
DB 661 RDSFTFTFLDLFKLTIGMDLEMLSTKYPVVFIIILTYIILTFVLLNMLIALMGE 720  
QY 721 TVGQVSKESKHIWKLOWATTIILDIERSFPVFLRAFRSGEMVTYVGSDDGTPDRRCFRV 780  
DB 721 TVGQVSKESKHIWKLOWATTIILDIERSFPVFLRAFRSGEMVTYVGSDDGTPDRRCFRV 780  
QY 781 DEVNWSHWNQNLGIINEDPGKNETYQYGFSGHTVGLRRDRWSSVPRVVELNKNKNPDE 840  
DB 721 DEVNWSHWNQNLGIINEDPGKNETYQYGFSGHTVGLRRDRWSSVPRVVELNKNKNPDE 840  
QY 841 VVPLDSMGNPCDGHQOQYPRKWRITDAP 870  
DB 781 VVPLDSMGNPCDGHQOQYPRKWRITDAP 810

## RESULT 13

US-09-764-367A-8

; Sequence 8, Application US/09764367A

; Patent No. US20020072101A1

; GENERAL INFORMATION:

```

; APPLICANT: Gaughan , Glen
; APPLICANT: Ramanathan, Chandra
; TITLE OF INVENTION: NOVEL HUMAN NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODING CAT
; TITLE OF INVENTION: CHANNELS
; FILE REFERENCE: 5624.252.999
; CURRENT APPLICATION NUMBER: US/09/764,367A
; PRIOR FILING DATE: 2001-01-18
; PRIOR FILING DATE: 60/177,554
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8
; LENGTH: 803
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-367A-8

Query Match          91.7%; Score 4199; DB 10; Length 803;
Best Local Similarity 99.5%; Pred. No. 5.1e-318;
Matches 798; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 69 MKQGAARKGVPNPIDLLLESTLYESSVPGPKAPMDSLFYGYRHHSSDNKRKKII 128
Db 1 MKQGAARKGVPNPIDLLLESTLYESSVPGPKAPMDSLFYGYRHHSSDNKRKKII 60

Qy 129 EKOQSPKAPAPPPPIIKVFNRPILFDIVSRGSTDGLDGLLPFLTHKKRLTDEEPREP 188
Db 61 EKOQSPKAPAPPPPIIKVFNRPILFDIVSRGSTDGLDGLLPFLTHKKRLTDEEPREP 120

Qy 189 STGKTCUPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOTALHIAIER 248
Db 121 STGKTCUPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOTALHIAIER 180

Qy 249 RCHHYVELLYVAQADVHAQARGRFQPKDEGGYFYFGEPLSLAACTNQPHVNYLTENP 308
Db 181 RCHHYVELLYVAQADVHAQARGRFQPKDEGGYFYFGEPLSLAACTNQPHVNYLTENP 240

Qy 309 HKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLFPDSNLEAVLNN 368
Db 241 HKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLFPDSNLEAVLNN 300

Qy 369 DGLSPLMAAATCKIGIFQHIIRREVTDTRHLSRKFKDWAYGVPVSSLYDLSLDTGC 428
Db 301 DGLSPLMAAATCKIGIFQHIIRREVTDTRHLSRKFKDWAYGVPVSSLYDLSLDTGC 360

Qy 429 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSVLCAMVIFTLT 488
Db 361 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSVLCAMVIFTLT 420

Qy 489 AYQPLEGTPPYPTTVDYLRAGEVITLFTGVLPFTTNIKDLFMKKCPGVNSLFDGSG 548
Db 421 AYQPLEGTPPYPTTVDYLRAGEVITLFTGVLPFTTNIKDLFMKKCPGVNSLFDGSG 480

Qy 549 FOLLYFYISVLIVSAALYLAGIEAYLAVMVFALVGLMMNALYFTRGLKLTGTYSIMIQ 608
Db 481 FOLLYFYISVLIVSAALYLAGIEAYLAVMVFALVGLMMNALYFTRGLKLTGTYSIMIQ 540

Qy 609 ILFKDLFRLLVLLFMIGYASALVSLNPNCAKMKVCNEQDNTCTVPTYPSCRDSEFTST 668
Db 541 ILFKDLFRLLVLLFMIGYASALVSLNPNCAKMKVCNEQDNTCTVPTYPSCRDSEFTST 600

Qy 669 FLDLRLKLTGMGDMLESTKYPVVFIIILTVYIILTVLLNMLIALMGETVGVQSKE 728
Db 601 FLDLRLKLTGMGDMLESTKYPVVFIIILTVYIILTVYIILTVLLNMLIALMGETVGVQSKE 660

Qy 729 SKHIWKLOWATTIILDIERSPPVFLRKAFRSGEMVTVGKSSDGTDRRCWCFRVDENNSHW 788
Db 661 SKHIWKLOWATTIILDIERSPPVFLRKAFRSGEMVTVGKSSDGTDRRCWCFRVDENNSHW 720

Qy 789 NONLGIINDEPGKNETYYGFSHTVGRRLRRDRSSVVPVRVELNKNNSNDEVVVPLDSM 848
Db 721 NONLGIINDEPGKNETYYGFSHTVGRRLRRDRSSVVPVRVELNKNNSNDEVVVPLDSM 780
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Qy 849 GNPRCDGHQOQGYPRKWRRTDDAP 870
Db 781 GNPRCDGHQOQGYPRKWRRTDDAP 802

RESULT 14
US-09-764-367A-2
; Sequence 2, Application US/09764367A
; Patent No. US20020072101A1
; GENERAL INFORMATION:
; APPLICANT: Gaughan , Glen
; APPLICANT: Ramanathan, Chandra
; TITLE OF INVENTION: NOVEL HUMAN NUCLEIC ACID MOLECULES AND POLYPEPTIDES ENCODI
; TITLE OF INVENTION: CHANNELS
; FILE REFERENCE: 5624.252.999
; CURRENT APPLICATION NUMBER: US/09/764,367A
; CURRENT FILING DATE: 2001-01-18
; PRIOR FILING DATE: 60/177,554
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-367A-2

Query Match          90.4%; Score 4138; DB 10; Length 792;
Best Local Similarity 98.8%; Pred. No. 3e-313;
Matches 790; Conservative 0; Mismatches 2; Indels 8; Gaps 1;

Qy 69 MKQGAARKGVPNPIDLLLESTLYESSVPGPKAPMDSLFYGYRHHSSDNKRKKII 128
Db 1 MKQGAARKGVPNPIDLLLESTLYESSVPGPKAPMDSLFYGYRHHSSDNKRKKII 60

Qy 129 EKOQSPKAPAPPPPIIKVFNRPILFDIVSRGSTDGLDGLLPFLTHKKRLTDEEPREP 188
Db 61 EKOQSPKAPAPPPPIIKVFNRPILFDIVSRGSTDGLDGLLPFLTHKKRLTDEEPREP 120

Qy 189 STGKTCUPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOTALHIAIER 248
Db 121 STGKTCUPKALLNSGRNDTIPVLLDIAERTGNMREFINSPFRDIYRGOTALHIAIER 180

Qy 249 RCHHYVELLYVAQADVHAQARGRFQPKDEGGYFYFGEPLSLAACTNQPHVNYLTENP 308
Db 181 RCHHYVELLYVAQADVHAQARGRFQPKDEGGYFYFGEPLSLAACTNQPHVNYLTENP 240

Qy 309 HKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLFPDSNLEAVLNN 368
Db 241 HKADMRQDSRGNTVLHALVAIADNTRENTKFTVMYDILLKLCARLFPDSNLEAVLNN 300

Qy 369 DGLSPLMAAATCKIGIFQHIIRREVTDTRHLSRKFKDWAYGVPVSSLYDLSLDTGC 428
Db 301 DGLSPLMAAATCKIGIFQHIIRREVTDTRHLSRKFKDWAYGVPVSSLYDLSLDTGC 360

Qy 429 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSVLCAMVIFTLT 488
Db 361 EASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVSVLCAMVIFTLT 420

Qy 489 AYQPLEGTPPYPTTVDYLRAGEVITLFTGVLPFTTNIKDLFMKKCPGVNSLFDGSG 548
Db 421 AYQPLEGTPPYPTTVDYLRAGEVITLFTGVLPFTTNIKDLFMKKCPGVNSLFDGSG 480

Qy 549 FOLLYFYISVLIVSAALYLAGIEAYLAVMVFALVGLMMNALYFTRGLKLTGTYSIMIQ 608
Db 481 FOLLYFYISVLIVSAALYLAGIEAYLAVMVFALVGLMMNALYFTRGLKLTGTYSIMIQ 540

Qy 609 ILFKDLFRLLVLLFMIGYASALVSLNPNCAKMKVCNEQDNTCTVPTYPSCRDSEFTST 668
Db 541 ILFKDLFRLLVLLFMIGYASALVSLNPNCAKMKVCNEQDNTCTVPTYPSCRDSEFTST 600

Qy 669 FLDLRLKLTGMGDMLESTKYPVVFIIILTVYIILTVLLNMLIALMGETVGVQSKE 728
Db 721 FLDLRLKLTGMGDMLESTKYPVVFIIILTVYIILTVLLNMLIALMGETVGVQSKE 728
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Db 601 FLDLFKLTIGMGDLEMLSSTKYPVVFILLVTVIILTFVLLLNMLIALMGETVQVSK 660  
Qy 729 SKHIWKLOWATTIILDIERSPVFLRKAFRSGEMTVGKSSDGTDDRWCRCFVDEVNWSHW 788  
Db 661 SKHIWKLOWATTIILDIERSPVFLRKAFRSGEMTVGKSSDGTDDRWCRCFVDEVNWSHW 720  
Qy 789 NONLGIINEDPGKNETQYGFSTVGRRLRRDRSSVVPVVELNKNKNPDEVVVPDLSM 848  
Db 721 NONLGIINEDPGKNETQYGFSTVGRRLRRDRSSVVPVVELNKNKNPDEVVVPDLSM 772  
Qy 849 GNPRCDGHQOQYPRKWRD 868  
Db 773 GNPRCDGHQOQYPRKWRD 792

## RESULT 15

US-10-027-828-6  
: Sequence 6, Application US/10027828  
: Publication No. US20030013650A1  
: GENERAL INFORMATION:  
: APPLICANT: Liedtke, Wolfgang  
: APPLICANT: Heller, Stefan  
: APPLICANT: Hudspeth, Albert J.  
: APPLICANT: Friedman, Jeffrey M.  
: TITLE OF INVENTION: VR-OAC, AN OSMOTICALLY ACTIVATED CHANNEL PROTEIN, NUCLEIC ACIDS  
: TITLE OF INVENTION: IT AND USES THEREOF  
: FILE REFERENCE: 600-1-287N  
: CURRENT APPLICATION NUMBER: US/10/027,828  
: CURRENT FILING DATE: 2001-10-25  
: PRIOR APPLICATION NUMBER: US 60/243,568  
: PRIOR FILING DATE: 2000-10-26  
: NUMBER OF SEQ ID NOS: 20  
: SOFTWARE: PatentIn version 3.1  
: SEQ ID NO 6  
: LENGTH: 830  
: TYPE: PRT  
: ORGANISM: Rattus norvegicus  
US-10-027-828-6

Query Match 90.2%; Score 4127.5; DB 9; Length 830;  
Best Local Similarity 90.0%; Pred. No. 2.1e-312;  
Matches 783; Conservative 23; Mismatches 23; Indels 41; Gaps 1;  
Qy 1 MADSSCPGAGCEVAELPCDESGTTCGGEAPFLSSLANLFEDEGSLSPSPADASRACP 60  
Db 1 MADPGDGPRAAPGDVAEPDGGESGTTCGGEAPFLSSLANLFEDEGSLSPSPADASRACP 60  
Qy 61 GDGRPNLRMKFQGAFRKGVNPNIDLLESTLYESSVYVPGPKAPMDSLFDTYRHHSSDN 120  
Db 61 GDGRPNLRMKFQGAFRKGVNPNIDLLESTLYESSVYVPGPKAPMDSLFDTYRHHSSDN 120  
Qy 121 KWRKKIIEKQOSPKAPAPQPPPIILKVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180  
Db 121 KWRKKVVEKQOSPKAPAPQPPPIILKVFNRPILFDIVSRGSTADLDGLLPFLTHKKRL 180  
Qy 181 TDEEFREPSTGKCLPKALLNLNGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
Db 181 TDEEFREPSTGKCLPKALLNLNGRNDTIPVLLDIAERTGNMREFINSFPRDIYRGQT 240  
Qy 241 ALHIAIERCKHYVELLVAGADVHAQAGRRFPQKDEGGYFYFGEPLSLAACTNPHI 300  
Db 241 ALHIAIERCKHYVELLVAGADVHAQAGRRFPQKDEGGYFYFGEPLSLAACTNPHI 300  
Qy 301 VNYLTENPHKKDMRRQDSRGNTVLHALVAIAIDNTRENTKFTVKMYDILLKCARLPDPS 360  
Db 301 VNYLTENPHKKDMRRQDSRGNTVLHALVAIAIDNTRENTKFTVKMYDILLKCARLPDPS 360  
Qy 361 NLEAVLNNDGLSPLMAAKTGKIGFQHIIRREVTDETRHLSRKFQDWAGYGPVYSSLYD 420  
Db 361 NLEAVLNNDGLSPLMAAKTGKIGFQHIIRREVTDETRHLSRKFQDWAGYGPVYSSLYD 420  
Qy 421 LSSLDTCGBEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480

Db 421 LSSLDTCGBEASVLEILVYNSKIENRHEMLAVEPINELLRDKWRKFGAVSFYINVVSYLC 480  
Qy 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFVFTTNIKDLEMKKCPGV 540  
Db 481 AMVIFTLTAYYQPLEGTPPYRTVDYLRAGEVITLFTGVLFVFTTNIKDLEMKKCPGV 540  
Qy 541 NSLFIDGSGFOLLFYIYSVLIVSAALYLAGIEAYLAYVWFALVGLWNNALYFTTGLKLTG 600  
Db 541 NSLFIDGSGFOLLFYIYSVLIVSAALYLAGIEAYLAYVWFALVGLWNNALYFTTGLKLTG 600  
Qy 601 TYSIMIOKILFKDLFRELLVYLLFMIGYASALYSLNPNCANMKVCNEDQNTCTVPTVPS 660  
Db 601 TYSIMIOKILFKDLFRELLVYLLFMIGYASALYSLNPNCANMKVCNEDQNTCTVPTVPS 660  
Qy 661 RDSETFSTFLDLFKLTIGMGDLEMLSSTKYPVVFILLVTVIILTFVLLLNMLIALMG 720  
Db 661 RDSETFSAFLDLFKLTIGMGDLEMLSSAKYPVVFILLVTVIILTFVLLLNMLIALMG 720  
Qy 721 TVGOVSKESKHINKLOWATTIILDIERSFPVFLRKAFRSGEMTVGKSSDGTDDRWCRCF 780  
Db 721 TVGOVSKESKHINKLOWATTIILDIERSFPVFLRKAFRSGEMTVGKSSDGTDDRWCRCF 780  
Qy 781 DEYNWSHWNONLGIINEDPGKNETQYGFSTVGRRLRRDRSSVVPVVELNKNKNPDE 840  
Db 741 -QYNWSHWNONLGIINEDPGKSEIYQYGFSTVGRRLRRDRSSVVPVVELNKNKSGTDE 799  
Qy 841 VVYPLDSMGNPRCDGHQOQYPRKWRD 870  
Db 800 VVYPLDNLGNPNCDGHQOQYAPKWRAD 829

Search completed: June 3, 2003, 19:57:03  
Job time : 32 secs